

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:10:39 ; Search time 549.862 Seconds
(without alignments)
2453.577 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700

Sequence: 1 QVQLQSGAGLEKKPGESLKI.....AKMPEYFGHMGCTIVTVSS 129

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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13: geneseqn2004bs: *
14: geneseqn2005s: *
15: geneseqn2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	700	100.0	765	6 AAD32664	Aad32664 Chimeric
2	697	99.6	774	2 AAT50787	Aat50787 C6 human
3	694	99.1	807	6 AAD32665	Aad32665 Chimeric

4	694	99.1	846	6 AAD32666	Aad32666 Chimeric
5	694	99.1	861	6 AAD32667	Aad32667 Chimeric
6	694	99.1	873	6 AAD32669	Aad32669 Chimeric
7	694	99.1	888	6 AAD32668	Aad32668 Chimeric
8	629	89.9	387	4 AAS03465	Aas03465 DNA encod
9	540	77.7	364	15 AEE03776	Aee03776 Antibody
10	540	77.1	906	5 AAF61513	Aaf61513 DNA encod
11	539	77.0	369	14 AEB01074	Aeb01074 Human IP1
12	534.5	76.4	660	10 AEB74803	Abz74803 Human ant
13	532.5	76.1	666	10 AEB74798	Abz74798 Human ant
14	532.5	76.1	666	10 AEB74810	Abz74810 Human ant
15	532.5	76.1	672	10 AEB74813	Abz74813 Human ant
16	531	75.9	669	10 AEB74791	Abz74791 Human ant
17	530.5	75.8	379	10 AAD18645	Adk18645 Anti-huma
18	530.5	75.8	379	12 ADL25423	Adl25423 Human mAb
19	529	75.6	669	10 AEB74812	Abz74812 Human ant
20	528.5	75.5	379	10 AAD18653	Adk18653 Anti-huma
21	528.5	75.5	379	10 AAD18641	Adk18641 Anti-huma
22	528.5	75.5	379	12 ADL25439	Adl25439 Human mAb
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24	528.5	75.5	666	10 AEB74804	Abz74804 Human ant
25	528	75.4	730	3 AA229000	Aaz29000 Anti-mur
26	527.5	75.4	438	4 AA41155	Aah41155 Human cod
27	527	75.3	351	6 AAL43585	Aal43585 Dlg1 anti
28	527	75.3	351	8 ACC47597	Acc47597 Human ant
29	526.5	75.2	666	10 AEB74799	Abz74799 Human ant
30	526.5	75.2	672	10 AEB74793	Abz74793 Human ant
31	526	75.1	369	13 ADS19292	Ads19292 Heavy cha
32	526	75.1	669	10 AEB74800	Abz74800 Human ant
33	525	75.0	669	10 AEB74807	Abz74807 Human ant
34	524	74.9	357	10 ADD69255	Add69255 Human ant
35	523.5	74.8	379	10 AAD18664	Adk18664 Anti-huma
36	523.5	74.8	379	12 ADL25459	Adl25459 Human mAb
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40	520	74.3	462	2 AAT73442	Aat73442 Human imm
41	520	74.3	462	2 AAV39240	Aav39240 Functional
42	520	74.3	462	2 AAZ21994	Aaz21994 Partial n
43	519	74.1	351	15 AEB24185	Aeb24185 Human INF
44	519	74.1	351	15 AEB24186	Aeb24186 Human INF
45	519	74.1	469	8 AAD56222	Aad56222 Human AB-
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ALIGNMENTS

RESULT 1	
AAD32664	
ID	AAD32664 standard; DNA: 765 BP.
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AC	AAD32664;
XX	
DT	29-AUG-2003 (revised)
DT	18-JUN-2002 (first entry)
XX	
DE	Chimeric SCBP C6.5 sfv DNA.
XX	
KW	Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
KW	nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
KW	gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX	
OS	Homo sapiens.
OS	Mus sp.
OS	Chimeric.
XX	
FH	Key
FT	CDS
FT	1..765
FT	/tag= a
FT	/product= "Chimeric SCBP C6.5 sfv protein"
FT	/note= "CDS does not include start and stop codon"
XX	/partial
PN	MO200200914-A2.

XX 03-JAN-2002.
 PD 25-JUN-2001; 2001WO-US020182.
 XX 23-JUN-2000; 2000US-0213653P.
 XX (HUST/) HUSTON J S.
 PA (WILS/) WILS P.
 PA (OJAN/) OJAN Z.
 PA (LAUR/) LAURENT O.
 PA (MARA/) MARASCO W A.
 PA (SCHE/) SCHERMAN D.
 XX Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
 XX WPI; 2002-268789/31.
 DR P-PSDB; AAE20407.
 XX
 PT Gene-delivery compound for targeted gene delivery, comprises single-chain
 PT binding polypeptide having effector segment with cysteinyl residue and
 PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
 PT residue.
 XX
 PS Disclosure: Fig 4; 96pp; English.
 XX
 CC The invention relates to gene-delivery compound comprising a single-chain
 CC binding polypeptide (SCBP) having at least one effector segment having a
 CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
 CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
 CC compound is useful for targeted gene delivery for treating diseases by
 CC gene therapy. The present sequence is chimeric SCBP C6.5 sFV DNA
 CC comprising human and murine sequences. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 765 BP; 155 A; 217 C; 227 G; 166 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,31e-64 Length: 765
 Score: 700.00 Matches: 129
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

US-10-092-640-32 (1-129) x AAD32664 (1-765)

QY 1 glnvalglnleuleuglnsergiyalagiuleulylsproglygluserleuylsile 20
 DB 1 CAGGTGCACACTGTTGCAGTCTGGCGCAGAGTTGAAAAACCGGGGAGTCTCGAAGATC 60
 QY 21 sercyglyglyserglytyrserphenrsertrytrp11ealatrvalarginmet 40
 DB 61 tccctgaaaggttcttgatracagctttaccagcttgcggtccctggggcccgacagtg 120
 QY 41 proglylvglyleuenglurtyrmetgylleuilletytrproglyaspserasprthlystyr 60
 DB 121 cccgggaaagccctggagtracatggggctcatatcctgggactcttgacacacaaatgc 180
 QY 61 serproserpheglnlyglnvalthrileservalasplyservalserthralatyr 80
 DB 181 accccgctcttccaaagccagcagctcacatctcagtcagacaagtcgctcagcactgcctac 240
 QY 81 leuqlttrpserserleulylproseraspseralvaltyrphecysalaarghisasp 100
 DB 241 ttgcataatgagcagcttgcgaagccctcgacagccgctgataattttgtgcgacacatgac 300
 QY 101 valgltyrcysersersersersasysalalvestrproglylurpheglnhistrpgly 120
 DB 301 ggaggatattgacgltgattccaaactgcggcaaaatggcctgaaatccttcagacattggggc 360
 QY 121 glnglythrleuvalthrvalser 129
 DB |||||

DB 361 CAGGGACCCCTGTCACGCTCTCTCA 387

RESULT 2

AAT50787
 ID AAT50787 standard; DNA; 774 BP.

AC AAT50787;

DT 23-SEP-1997 (first entry)

DE C6 human sFV antibody C6.5 encoding DNA.

KW Tumour; immune response; cytotoxin; carcinoma; breast cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..774

FT /product= "Antibody C6.5"

FT /transl_except= (pos: 181..183, aa: Ser)

FT /transl_except= (pos: 361..363, aa: Gly)

FT /note= "Without stop codon"

PN WO9700271-A1.

PD 03-JAN-1997.

PF 13-JUN-1996; 96WO-US010287.

PR 14-JUN-1995; 95US-0000238P.

PR 15-JUN-1995; 95US-0000250P.

PA (REGC) UNIV CALIFORNIA.

PI Marke JD, Schler R;

DR WPI; 1997-077488/07.

DR P-PSDB; AAM08487.

PT New C6 human antibody binding specifically to c-erbB-2 - useful for

PT treatment and diagnosis of tumours, with reduced risk of generating

PT immune response.

PT Claim 4; Fig 1; 117pp; English.

PS The present sequence encodes a C6 human antibody C6.5, that binds

CC specifically to c-erbB-2. A chimeric molecule that binds specifically to

CC tumour cells carrying c-erbB-2 consists of an effector compound attached

CC to a C6 human antibody, e.g. C6.5. If the effector compound is a

CC cytotoxin the chimeric molecule can be used to inhibit growth of c-erbB-2

CC positive tumours (especially breast and other carcinomas). If the

CC effector compound is a label the chimeric molecule can be used to detect

CC such cells, including in vivo localisation. The antibody can also be used

CC for diagnosis/localisation, in vivo or in vitro, especially by

CC immunoassay. The nucleic acid encoding the antibody, and a nucleic acid

CC encoding a single chain polypeptide with the binding specificity of the

CC antibody and comprising the binding portions of variable regions of light

CC and heavy chains of the antibody, joined by a linker, can be used to

CC produce recombinant proteins by standard methods. Unlike known anti-c-

CC erbB-2 antibodies, C6 antibodies are fully human, so should elicit

CC little, if any, immunogenic response

SQ Sequence 774 BP; 156 A; 222 C; 230 G; 166 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.05e-64 Length: 774
 Score: 697.00 Matches: 128
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 99.2% Mismatches: 0
 Query Match: 99.6% Indels: 0
 DB: Gaps: 0

US-10-092-640-32 (1-129) x AAT50787 (1-774)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
 Db 1 CAGGTCACTGTTGTCAGTCTGGGCGAGAGTTGAAAAAAGCCGGGAGTCTCGAAGATC 60
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
 Db 61 TCCTGTAAAGGTTCTGATACAGCTTACCACTGATCCCTGGGTCGCCCGCAGATG 120
 QY 41 ProGlyLysGlyLeuGlnLutyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
 Db 121 CCGGGAAAGGCTTGAGATACATGGAGCTCATTTATCTGGTACTCTGCACCAATATC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 181 ACGCCGCTCTTCCAAAGCCAGGTCACCATCTCAGTGCAGAACGTCCTCAGCACTGCTAC 240
 QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 Db 241 TTGCATATGAGACAGTCTGAAGCCCTCGACAGCGCCGTGATTTTGTGCGAGACATGAC 300
 QY 101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTrpProGlyLutyrPheGlnHisTrpGly 120
 Db 301 GTGGGATATTGTCAGTATGTTCCAACTGCGCAAGTGGCTGAATACTTCCAGCATTTGGGC 360
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 Db 361 CAGGGCACCCCTGTCTCAGCTCTCTCTCA 387

RESULT 3

AAD32665
 ID AAD32665 standard; DNA; 807 BP.

XX AAD32665;

AC 29-AUG-2003 (revised)
 DT 18-JUN-2002 (first entry)

XX Chimeric SCBP C6ML3-9 sFV' DNA.

XX Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
 KM nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
 KM gene therapy; targeted gene delivery; human; murine; chimeric; ds.

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

XX Key

FT CDS Location/Qualifiers
 FT 1..807
 FT /tag= a
 FT /product= "Chimeric SCBP C6ML3-9 sFV' protein"
 FT /note= "CDS does not include start and stop codon"
 FT /partial

XX WO200200914-A2.

XX 03-JAN-2002.

XX 25-JUN-2001; 2001WO-US020182.

XX 23-JUN-2000; 2000US-0213653P.

XX (HUST/) HUSTON J S.

XX (WILS/) WILS P.

XX (QUAN/) QUAN Z.

XX (LAUR/) LAURENT O.

XX (MARA/) MARASCO W A.

XX (SCHE/) SCHERMAN D.

XX Huson JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;

XX MPI; 2002-268789/31.

XX Gene-delivery compound for targeted gene delivery, comprises single-chain
 PT binding polypeptide having effector segment with cysteinyl residue and
 PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
 PT residue.

XX Disclosure; Fig 6; 96pp; English.

XX The invention relates to gene-delivery compound comprising a single-chain
 CC binding polypeptide (SCBP) having at least one effector segment having a
 CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
 CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
 CC compound is useful for targeted gene delivery for treating diseases by
 CC gene therapy. The present sequence is chimeric SCBP C6ML3-9 sFV' DNA
 CC comprising human and murine sequences. (Updated on 29-AUG-2003 to
 CC standardise OS field)

XX SQ Sequence 807 BP; 160 A; 240 C; 237 G; 170 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:
1..97e-63	807	694.00	127
Percent Similarity:		100.0%	
Best Local Similarity:		98.4%	
Query Match:		99.1%	
DB:		Gaps:	0

US-10-092-640-32 (1-129) x AAD32665 (1-807)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
 Db 1 CAGGTCACTGTTGTCAGTCTGGGCGAGAGTTGAAAAAAGCCGGGAGTCTCGAAGATC 60
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
 Db 61 TCCTGTAAAGGTTCTGATACAGCTTACCACTGATCCCTGGGTCGCCCGCAGATG 120
 QY 41 ProGlyLysGlyLeuGlnLutyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
 Db 121 CCGGGAAAGGCTTGAGATACATGGAGCTCATTTATCTGGTACTCTGCACCAATATC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 181 ACGCCGCTCTTCCAAAGCCAGGTCACCATCTCAGTGCAGAACGTCCTCAGCACTGCTAC 240
 QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 Db 241 TTGCATATGAGACAGTCTGAAGCCCTCGACAGCGCCGTGATTTTGTGCGAGACATGAC 300
 QY 101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTrpProGlyLutyrPheGlnHisTrpGly 120
 Db 301 GTGGGATATTGTCAGTATGTTCCAACTGCGCAAGTGGCTGAATACTTCCAGCATTTGGGC 360
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 Db 361 CAGGGCACCCCTGTCTCAGCTCTCTCTCTCA 387

RESULT 4

AAD32666
 ID AAD32666 standard; DNA; 846 BP.

XX AAD32666;

XX 29-AUG-2003 (revised)

XX 18-JUN-2002 (first entry)

XX Chimeric SCBP C6ML-3-sFV' -L1-KDEL DNA.

XX Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
 KM nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
 KM gene therapy; targeted gene delivery; human; murine; chimeric; ds.

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XX OS Homo sapiens.
OS Mus sp.
OS Chimeric.
FH Key Location/Qualifiers
FT CDS 1..846
FT /tag= a
FT /product= "Chimeric SCBP C6ML-3-9sFv'-L1-KDEL protein"
FT /note= "CDS does not include start and stop codon"
FT /partial

XX PN MO200200914-A2.
XX PD 03-JAN-2002.
XX PF 25-JUN-2001; 2001WO-US020182.
XX PR 23-JUN-2000; 2000US-0213653P.
XX PA (HUST/) HUSTON J S.
XX PA (WILS/) WILS P.
XX PA (QUAN/) QUAN Z.
XX PA (LAUR/) LAURENT O.
XX PA (MARA/) MARASCO W A.
XX PA (SCHE/) SCHERMAN D.
XX PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D,
XX DR WPI; 2002-268789/31.
XX DR P-PSDB; AAE20409.
XX PT Gene-delivery compound for targeted gene delivery, comprises single-chain
XX PT binding polypeptide having effector segment with cysteinyl residue and
XX PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
XX PT residue.
XX PS Example 2; Fig 8; 96pp; English.
XX CC The invention relates to gene-delivery compound comprising a single-chain
XX CC binding polypeptide (SCBP) having at least one effector segment having a
XX CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
XX CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
XX CC compound is useful for targeted gene delivery for treating diseases by
XX CC gene therapy. The present sequence is chimeric SCBP C6ML-3-9sFv'-L1-KDEL
XX CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
XX CC standardise OS field)
XX SQ Sequence 846 BP; 171 A; 250 C; 246 G; 179 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,09e-63 Length: 846
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 6 Gaps: 0

US-10-092-640-32 (1-129) x AAD32666 (1-846)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLeuYsProGlyGluSerLeuLeuYsile 20
DB 1 CAGGTCACACTGCTGTCAGTCTGGGGCAGAGGTAAATAACCCCGGAGTCTCTGAAGATC 60
QY 21 SerGlySlyGlySerGlyTyrSerPheThrSerTyrTyrIleAlaTyrValArgGlnMet 40
DB 61 TCTGTAAAGGGTTCGTGATACAGCTTACACAGCTACTGATCGCTGGGTGCGCCAGATG 120
QY 41 ProGlySlyGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerThrIleTyr 60
DB 121 CCCGGGAAAGGCTTGAGTACACAGGGGGCTCATCTATCTGCTGATCTACACCAATATAC 180
QY 61 SerProSerPheGlnGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80

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DB 181 ACCCGCTCTTCCAAAGGCCAGGTCAACCATCTAGTCGACAGTCCGTCAGCATGCTCAC 240
QY 81 LeuGlnTyrPheSerLeuLeuYsProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
DB 241 TTGCATATGAGCAGTCTGAGAGCCCTCGGACAGCGCCGTGTATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB 301 GTGGATATTGTCAGTATTCACATGCGCAAGTGGCCGTAATACTTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGCACCCCTGCTGTCACCTCTCTCA 387

RESULT 5
AAD32667
ID AAD32667 strand; DNA; 861 BP.
XX
XX AAD32667;
XX AC 29-AUG-2003 (revised)
XX DT 18-JUN-2002 (first entry)
XX DE Chimeric SCBP C6ML-3-9sFv'-L2-KDEL DNA.
XX KW Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
XX KW nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
XX KW gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX OS Homo sapiens.
XX OS Mus sp.
XX OS Chimeric.
FH Key Location/Qualifiers
FT CDS 1..861
FT /tag= a
FT /product= "Chimeric SCBP C6ML-3-9sFv'-L2-KDEL protein"
FT /note= "CDS does not include start and stop codon"
FT /partial

XX PN WO200200914-A2.
XX PD 03-JAN-2002.
XX PF 25-JUN-2001; 2001WO-US020182.
XX PR 23-JUN-2000; 2000US-0213653P.
XX PA (HUST/) HUSTON J S.
XX PA (WILS/) WILS P.
XX PA (QUAN/) QUAN Z.
XX PA (LAUR/) LAURENT O.
XX PA (MARA/) MARASCO W A.
XX PA (SCHE/) SCHERMAN D.
XX PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D,
XX DR WPI; 2002-268789/31.
XX DR P-PSDB; AAE20410.
XX PT Gene-delivery compound for targeted gene delivery, comprises single-chain
XX PT binding polypeptide having effector segment with cysteinyl residue and
XX PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
XX PT residue.
XX PS Example 2; Fig 10; 96pp; English.
XX CC The invention relates to gene-delivery compound comprising a single-chain
XX CC binding polypeptide (SCBP) having at least one effector segment having a
XX CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
XX CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
XX CC compound is useful for targeted gene delivery for treating diseases by

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CC Gene therapy. The present sequence is chimeric SCBP C6ML-3-9sFV'-L2-KDEL
 CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
 CC standardise OS field)

XX SQ Sequence 861 BP; 173 A; 255 C; 250 G; 183 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,13e-63	Length:	861
Score:	694.00	Matches:	127
Percent Similarity:	100.0%	Conservative:	2
Best Local Similarity:	98.4%	Mismatches:	0
Query Match:	99.1%	Indels:	0
DB:	6	Gaps:	0

US-10-092-640-32 (1-129) x AAD32667 (1-861)

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OY 1 GlnValGlnLeuLeuGlnSerGlnValGlnLeuLeuLeuProGlnGlnSerLeuLeuIle 20
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DB 1 CAGGTGCAGCTGCTGCAAGTCTGGGGCAGAGGTAAAGCCGGGAGTCTCGAAGATC 60
OY 21 SerCySLySGlySerGlyTySerPheThrSerTyTrpIleAlaTrpValArgGlnMet 40
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DB 61 TCCTGTAAAGGTTCTGATACAGCTTACCACTGATCGCTGGGTGCCAGATG 120
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DB 121 CCGGGAAAGGCTGAGTACATGGGGCTCATATCTGCTGACTGACACCAATAC 180
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DB 181 AGCCGCTCTTCCAAAGCCAGGTCACATCTCAGTGCAGACAGCCGTCAGACTGCTAC 240
OY 81 LeuGlnTrpSerSerLeuLeuProSerAspSerAlaValTyPheCysAlaArgHisAsp 100
    |||||
DB 241 TTGCATGAGAGCAGTCTGAAGCCCTCGACAGCGCGGTATTTGTGGAGACATGAC 300
OY 101 ValGlyTyCySerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
    |||||
DB 301 GTGGGATATTGCAAGTTCACACTGCGAAAGTGGCTGAAATATTCCAGCATTTGGGGC 360
OY 121 GlnGlyThrLeuValThrValSerSer 129
    |||||
DB 361 CAGGGCACCTGCTGCTCCTCTCA 387

```

RESULT 6

AAD32669 standard; DNA; 873 BP.

XX AAD32669;

XX 29-AUG-2003 (revised)

XX 18-JUN-2002 (first entry)

XX Chimeric SCBP C6ML-3-9sFV'-L2-nls DNA.

XX Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;

XX nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;

XX gene therapy; targeted gene delivery; human; murine; chimeric; ds.

XX Homo sapiens.

XX Mus sp.

XX Chimeric.

XX Key

XX CDS

XX Location/Qualifiers

XX 1..873

XX /tag= a

XX /product= "Chimeric SCBP C6ML-3-9sFV'-L2-nls protein"

XX /note= "CDS does not include start and stop codon"

XX /partial

XX WO200200914-A2.

XX 03-JAN-2002.

XX 25-JUN-2001; 2001WO-US020182.
 XX 23-JUN-2000; 2000US-0213653P.

XX (HUST/) HUSTON J S.

XX (WILS/) WILS P.

XX (QUAN/) QUAN Z.

XX (LAUR/) LAURENT O.

XX (MARA/) MARASCO W A.

XX (SCHE/) SCHERMAN D.

XX Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;

XX WPI; 2002-268789/31.

XX P-PSDB; AAE20412.

XX Gene-delivery compound for targeted gene delivery, comprises single-chain

XX binding polypeptide having effector segment with cysteinyl residue and

XX nucleic acid-binding/lipid-associating moiety coupled to polypeptide by

XX residue.

XX Example 2; Fig 14; 96pp; English.

XX The invention relates to gene-delivery compound comprising a single-chain

XX binding polypeptide (SCBP) having at least one effector segment having a

XX cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-

XX associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery

XX compound is useful for targeted gene delivery for treating diseases by

XX gene therapy. The present sequence is chimeric SCBP C6ML-3-9sFV'-L2-nls

XX DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to

XX standardise OS field)

XX SQ Sequence 873 BP; 177 A; 260 C; 252 G; 184 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	2,17e-63	Length:	873
Score:	694.00	Matches:	127
Percent Similarity:	100.0%	Conservative:	2
Best Local Similarity:	98.4%	Mismatches:	0
Query Match:	99.1%	Indels:	0
DB:	6	Gaps:	0

US-10-092-640-32 (1-129) x AAD32669 (1-873)

```

OY 1 GlnValGlnLeuLeuGlnSerGlnValGlnLeuLeuLeuProGlnGlnSerLeuLeuIle 20
    |||||
DB 1 CAGGTGCAGCTGCTGCAAGTCTGGGGCAGAGGTAAAGCCGGGAGTCTCGAAGATC 60
OY 21 SerCySLySGlySerGlyTySerPheThrSerTyTrpIleAlaTrpValArgGlnMet 40
    |||||
DB 61 TCCTGTAAAGGTTCTGATACAGCTTACCACTGATCGCTGGGTGCCAGATG 120
OY 41 ProGlnLySGlyLeuGlnTyMetGlyLeuIleTyProGlnLyAspSerAlaTrpValArgGlnMet 60
    |||||
DB 121 CCGGGAAAGGCTGAGTACATGGGGCTCATATCTGCTGACTGACACCAATAC 180
OY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLySerValSerThrAlaTyR 80
    |||||
DB 181 AGCCGCTCTTCCAAAGCCAGGTCACATCTCAGTGCAGACAGCCGTCAGACTGCTAC 240
OY 81 LeuGlnTrpSerSerLeuLeuProSerAspSerAlaValTyPheCysAlaArgHisAsp 100
    |||||
DB 241 TTGCATGAGAGCAGTCTGAAGCCCTCGACAGCGCGGTATTTGTGGAGACATGAC 300
OY 101 ValGlyTyCySerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
    |||||
DB 301 GTGGGATATTGCAAGTTCACACTGCGAAAGTGGCTGAAATATTCCAGCATTTGGGGC 360
OY 121 GlnGlyThrLeuValThrValSerSer 129
    |||||
DB 361 CAGGGCACCTGCTGCTCCTCTCA 387

```

```
RESULT 7
AAD32668
ID AAD32668 standard; DNA; 888 BP.
XX
AC AAD32668;
XX
DT 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
DE Chimeric SCBP C6ML-3-9sFv'-L2-H14 DNA.
XX
KW Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
KW nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
KW gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1..888
FT /tag=a
FT /product="Chimeric SCBP C6ML-3-9sFv'-L2-H14 protein"
FT /note="CDS does not include start and stop codon"
FT /partial
XX
PN WO200200914-A2.
XX
PD 03-JAN-2002.
XX
PF 25-JUN-2001; 2001WO-US020182.
XX
PR 23-JUN-2000; 2000US-0213653P.
XX
PA (HUST/) HUSTON J S.
PA (WILS/) WILS P.
PA (OUAN/) OUAN Z.
PA (LAUR/) LAURENT O.
PA (MARA/) MARASCO W A.
PA (SCHE/) SCHERMAN D.
XX
PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
DR MPI: 2002-268789/31.
DR P-PSDB; AAE20411.
XX
PT Gene-delivery compound for targeted gene delivery, comprises single-chain
PT binding polypeptide having effector segment with cysteinyl residue and
PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
PT residue.
XX
PS Example 2; Fig 12; 96pp; English.
XX
CC The invention relates to gene-delivery compound comprising a single-chain
CC binding polypeptide (SCBP) having at least one effector segment having a
CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
CC compound is useful for targeted gene delivery for treating diseases by
CC gene therapy. The present sequence is chimeric SCBP C6ML-3-9sFv'-L2-H14
CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 888 BP; 187 A; 263 C; 257 G; 181 T; 0 U; 0 Other;
Alignment Scores:
Pred. No. : 2,22e-63 Length: 888
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: Gaps: 0
US-10-092-640-32 (1-129) x AAD32668 (1-888)
```

```
QY 1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuLeuValProGlyGluSerLeuIysIle 20
Dbb 1 CAGGTGCAGCTGGTGCAGTCTGGGGCAGAGGAAAAAGCCCGGGGAGTCTCTGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrIserPheThrSerTyrTrpIleAlaTrpValArgGlnmet 40
Dbb 61 TCCTGTAAAGGGTTCGATATACAGCTTTACAGCTACTGGATGCGCTGGGTGGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrIlyTyr 60
Dbb 121 CCGGGGAAAGGCGCTGAGACATGGGGCTCATCTCTCTGGAGACTCTGACACCAAAATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Dbb 181 AGCCCGCTCTTCAGAGCCAGGTCAACATCTCAGTCGACAAAGTCCGTCAGCCTGCTTAC 240
QY 81 LeuGlnTyrPheSerSerLeuLysPheSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Dbb 241 TTGCAATGAGAGCAGTCTGAAGCCCTCGGACAGCGCGGTATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
Dbb 301 GTGGGATATTTGCAGATGTTCCAACTGCCCAAGTGGCTGAAATACCTTCAGCATTTGGGCG 360
QY 121 GlnGlyThrIleValThrValSerSer 129
Dbb 361 CAGGGCACCTGGTGCACCGTCTCTCA 387
RESULT 8
AAS03465
ID AAS03465 standard; cDNA; 387 BP.
XX
AC AAS03465;
XX
DT 29-AUG-2001 (first entry)
XX
DE DNA encoding anti-adipocyte monoclonal antibody heavy chain, FAT 53.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
KW heart disease; complementarity determining region; CDR; ss.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR MPI: 2001-282031/29.
DR P-PSDB; AAU02565.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
PS Disclosure; Page 133; 182pp; English.
XX
CC AAS03401-AAS03535 represent anti-adipocyte monoclonal antibody heavy and
CC light chain coding sequences of the invention. The antibodies can be used
CC in the treatment of obesity and obesity related diseases. The antibodies
CC can be used to deliver drugs or pro-drugs directly to the fat mass of an
CC obese patient or the antibody can be used as a therapeutic itself.
CC Antibodies binding specifically to adipocytes can be used to activate the
CC immune system to destroy the cells by complement mediated lysis. The
CC antibodies may be labeled with a detectable label such as radiolabel,
```

fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

Alignment Scores:

Pred. No.:	5,41e-57	Length:	387
Score:	629.00	Matches:	115
Percent Similarity:	95.3%	Conservative:	8
Best Local Similarity:	89.1%	Mismatches:	6
Query Match:	89.9%	Indels:	0
DB:	4	Gaps:	0

US-10-092-640-32 (1-129) x AAS03465 (1-387)

```
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLeuProGlyGlnSerLeuLysIle 20
    |||||
DB 1 CAGGTGACGCTGTTGACGTCTGGAGCAGAGTGAAGCCCGGAGACTCTCTGAAGATC 60
    |||||
QY 21 SerCysLeuGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgMet 40
    |||||
DB 61 TCCTGTAAGGCTTCTGGATTCACACTTCCCACTCTGGATCCGCTGGCGCCAGATG 120
    |||||
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerPheThrLysTyr 60
    |||||
DB 121 CCGGGAAGGCGCTCGAGTCAATGGGCTCATCTATCTGATGCTGACCAATAC 180
    |||||
QY 61 SerProSerPheGlnGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
    |||||
DB 181 AGCCGCTCTTCCAAAGCCGACACATGTCAGTCAAGTCCGTCAGACCTGCTAC 240
    |||||
QY 81 LeuGlnTrpSerSerLeuLysPheSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
    |||||
DB 241 TTGCATATGAGCAGCTGTGAGCCCTCGACAGCGCCCTGATTTTGTGTGAGACATGAC 300
    |||||
QY 101 ValGlyTyrCysSerSerSerSerAsnGlyAlaLysTrpProGlyTyrPheGlnHisTyrGly 120
    |||||
DB 301 GTGGGATATTGCGATGTTCCAACTGGCGCAAGAGGCGCTGAATCTTCCAGCATTTGGGCG 360
    |||||
QY 121 GlnGlyThrLeuValThrValSerSer 129
    |||||
DB 361 CGAGGAACCTGGTCAACCGTCTCTCA 387
    |||||
RESULT 9
ID AEE03776 standard; DNA; 364 BP.
AC AEE03776;
XX
XX 26-JUN-2006 (first entry)
XX
XX Antibody 015-126 VH nucleotide sequence SEQ ID NO:102.
XX
XX antibody production; cytostatic; diagnosis; cancer;
XX heavy chain variable region; coding sequence; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT 1..363
XX CDS /*tag= a
XX FT /partial
XX FT /product= "Antibody 015-126 VH amino acid sequence"
XX
XX JP2005185281-A.
XX
XX 14-JUL-2005.
```

XX 02-DEC-2004; 2004JP-00349783.
XX
XX 04-DEC-2003; 2003JP-00406554.
XX
XX (MBLV-) MBL VENTURE CAPITAL KK.
XX
XX Akabori Y, Sugioke A, Hayashi N, Morino K, Suzuki K, Morita Y;
XX Kurosawa H, Sumitomo M, Hamada S, Yakaaki A, Morino T, Kurosawa Y;
XX Miura K;
XX
XX WPI: 2006-022472/03.
XX P-PSDB; AEE03777.

XX Producing antibody binding to cell surface antigen, by contacting cell
XX expressing cell surface antigen and antibody library in aqueous medium,
XX transferring cell into low polar solvent phase of two phase system and
XX recovering antibody.

Example; SEQ ID NO 102; 89pp; Japanese.

XX The invention relates to a method (M1) for producing an antibody which
XX binds to a cell surface antigen. (M1) involves contacting a cell
XX expressing cell surface antigen on cytoplasmic membrane or its fraction
XX and an antibody library in an aqueous medium, preparing two phase system
XX consisting of aqueous medium and a low polar solvent, allowing the cell
XX to move into the low polar solvent phase and recovering cell or the
XX antibody which binds to the cell surface antigen from the solvent. (M1)
XX is useful for producing an antibody which binds to the cell surface
XX antigen. The antibody produced by (M1) is useful as a parameter e.g. a
XX diagnostic marker for diagnosing cancer. (M1) enables to screen for an
XX antibody, which binds to cell surface antigen specifically, rapidly and
XX reliably. The present sequence represents an antibody 015-126 VH
XX nucleotide sequence, which is used in the exemplification of the present
XX invention.

SQ Sequence 364 BP; 78 A; 100 C; 109 G; 77 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.14e-47	Length:	364
Score:	540.00	Matches:	101
Percent Similarity:	87.6%	Conservative:	12
Best Local Similarity:	76.3%	Mismatches:	8
Query Match:	77.1%	Indels:	1
DB:	15	Gaps:	1

US-10-092-640-32 (1-129) x AEE03776 (1-364)

```
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLeuProGlyGlnSerLeuLysIle 20
    |||||
DB 1 CAGGTGACGCTGTTGACGTCTGGAGCAGAGTGAAGCCCGGAGACTCTCTGAAGATC 60
    |||||
QY 21 SerCysLeuGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgMet 40
    |||||
DB 61 TCCTGTAAGGCTTCTGGATTCACACTTCCCACTCTGGATCCGCTGGCGCCAGATG 120
    |||||
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerPheThrLysTyr 60
    |||||
DB 121 CCGGGAAGGCGCTCGAGTCAATGGGCTCATCTATCTGATGCTGACCAATAC 180
    |||||
QY 61 SerProSerPheGlnGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
    |||||
DB 181 AGCCGCTCTTCCAAAGCCGACACATGTCAGTCAAGTCCGTCAGACCTGCTAC 240
    |||||
QY 81 LeuGlnTrpSerSerLeuLysPheSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
    |||||
DB 241 TTGCATATGAGCAGCTGTGAGCCCTCGACAGCGCCCTGATTTTGTGTGAGACATGAC 300
    |||||
QY 101 ValGlyTyrCysSerSerSerSerAsnGlyAlaLysTrpProGlyTyrPheGlnHisTyrGly 120
    |||||
DB 301 GTGGGATATTGCGATGTTCCAACTGGCGCAAGAGGCGCTGAATCTTCCAGCATTTGGGCG 336
    |||||
QY 121 GlnGlyThrLeuValThrValSerSer 129
    |||||
```

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Db          337 CAGGGAACCTGCTACCCGCTCTCGAGC 363
RESULT 10
AAF61513
ID          AAF61513 standard; DNA; 906 BP.
XX
XX          AAF61513;
AC
XX          11-SEP-2003 (revised)
DT          25-JUN-2001 (first entry)
XX
XX          DNA encoding SNV-env leader/human 6C3-scfv fusion construct.
DE
XX
XX          T lymphocyte; antibody; single chain variable antibody; scFv; human;
KM          cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KM          gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KM          acquired immune deficiency syndrome; severe combined immune deficiency;
KM          T cell lymphoma; fusion construct; ds.
XX
OS          Homo sapiens.
OS          Spleen necrosis virus.
OS          Chimeric.
FH
FT          Key          Location/Qualifiers
FT          CDS          1..135
FT                      +tag= a
FT                      /product= "SNV-env leader peptide"
FT                      /note= "No stop codon given"
FT          CDS          136..906
FT                      +tag= b
FT                      /product= "7B4-scfv"
FT                      /note= "no stop codon given"
FT                      /partial
XX
XX          DE19946142-A1.
XX
XX          29-MAR-2001.
XX
XX          27-SEP-1999; 99DE-01046142.
XX
XX          27-SEP-1999; 99DE-01046142.
XX
XX          (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
XX          Cichutek K, Engelstaedter M;
XX
XX          WPI; 2001-246140/26.
XX          P-PSDB; AAB70844.
XX
XX          Cell-targeting vector selective for T lymphocytes, useful in gene therapy
PT          of e.g. acquired immune deficiency syndrome, encodes a single-chain
PT          variable antibody fragment.
XX
XX          Claim 1, Fig 5; 18pp; German.
XX
XX          This invention describes a novel cell-targeting vector (A) containing a
CC          DNA sequence (1) encoding a single-chain variable antibody fragment
CC          (scFv). The products of the invention have antiviral, cytostatic and
CC          immunostimulant activity and can be used in gene therapy, immunization
CC          and diagnosis particularly of T cell-associated diseases, specifically
CC          acquired immune deficiency syndrome (AIDS), severe combined immune
CC          deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC          of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC          human B cells, and 1000 fold selectivity over other human cells. A vector
CC          designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC          fragment, fully defined in the specification. It was used to transform
CC          D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC          (SNV)) cells, C816 (human T lymphocyte) cells, and HeLa (human cervical
CC          carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC          determine transformation. The viral titer (infectious units/ml) was over
CC          1 million for D17, 1 million for C816 but less than 100 for HeLa,
CC          showing the high selectivity for human T cells. This sequence encodes the

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CC          SNV-env leader/human 6C3-scfv fusion construct used in the construction
CC          of novel cell targeting vectors described in the invention. (Updated on
CC          11-SEP-2003 to standardise OS field)
XX
XX          SQ          Sequence 906 BP; 204 A; 246 C; 262 G; 194 T; 0 U; 0 Other;
SQ
XX
XX          Alignment Scores:
XX          Pred. No.:          3,546-47          Length:          906
XX          Score:          540.00          Matches:          102
XX          Percent Similarity:          88.4%          Conservative:          12
XX          Best Local Similarity:          79.1%          Mismatches:          13
XX          Query Match:          77.1%          Indels:          2
XX          DB:          5          Gaps:          2
XX
XX          US-10-092-640-32 (1-129) x AAF61513 (1-906)
XX
XX          QY          1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuTlysProGlyGlnSerLeuTysIle 20
XX          |||||
XX          142 CAGGTACAGCTGCACAGTCAGAGACAGAAATGAAAAGCCCGGGAGCTCTGAAAATC 201
XX          |||||
XX          QY          21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
XX          |||||
XX          202 TCCTGTAAAGGGTTTGGATACGATCAGACTTACCTGATCGCTGGGTGGCCAGATG 261
XX          |||||
XX          QY          41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
XX          |||||
XX          262 CCGGGAAAGGCCCTGAGATCAGGGGCTCATCTTCTGGTACTTCGACCCAAATAC 321
XX          |||||
XX          QY          61 SerProSerPheGlnGlyAlaValThrIleSerValAspLysSerValSerThrAlaTyr 80
XX          |||||
XX          322 AGCCCGCTCTTCMAAGGCCAGGTCACCATCTCAGCGCAAGTCCATCGACGCCGCTAC 381
XX          |||||
XX          QY          81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
XX          |||||
XX          382 CTGCAGTGGACGAGCCTGAAAGCCTCGGACACCGCCATGTATCTACTACTACTACGACGCTCG 441
XX          |||||
XX          QY          101 ValGlyTyrCysSerSerSerAsnCysAlaTyrTrpProGlyTyrPheGlnHis--Tyr 119
XX          |||||
XX          442 ---GGATATTGTAGTAGTACACGCTGCTATGCTACTACTACTACTACTACGACGCTCG 498
XX          |||||
XX          QY          120 GlyGlnGlyThrLeuValThrValSer 128
XX          |||||
XX          499 GGCCGGGGAAACCTGCTGACCGCTCG 525
XX
XX          RESULT 11
XX          AEB01074
XX          ID          AEB01074 standard; DNA; 369 BP.
XX
XX          AEB01074;
AC
XX          08-SEP-2005 (first entry)
XX
XX          Human IP10 antibody heavy chain variable region DNA, SEQ ID NO 102.
XX
XX          antibody; IP-10; inflammation; immune disorder; dermatological disease;
KM          respiratory disease; neurological disease; degeneration; infection;
KM          neuroprotective; Antiarrhythmic; Antipneumatic; Antiinflammatory;
KM          Gastrointestinal-Gen.; Anticancer; Dermatological; Immunosuppressive;
KM          Antidiabetic; Antiproliferative; Antihypertensive; Antiasthmatic;
KM          Respiratory-Gen.; Cerebroprotective; Vasodilator; Nootropic;
KM          Antiparkinsonian; Antiangiogenic; Anticancerosclerotic; Virocide;
KM          Antibacterial; heavy chain variable region; ds; gene.
XX
XX          Homo sapiens.
XX
XX          WO2005058815-A2.
XX
XX          30-JUN-2005.
XX
XX          10-DEC-2004; 2004WO-US041506.
XX
XX          10-DEC-2003; 2003US-0529180P.
XX

```

PA (MEDA-) MEDAREX INC.
 XX Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
 PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;
 XX WPI: 2005-467095/47.
 DR P-PSDB; ABB01010.
 XX
 PT Isolated human monoclonal antibody or an antigen-binding portion, which
 PT specifically binds to human interferon gamma inducible protein 10 (IP-
 PT 10), useful for treating viral or bacterial infection, or inflammatory or
 PT autoimmune diseases.
 XX
 PS Disclosure; SEQ ID NO 102; 179pp; English.
 XX
 CC The invention relates to an isolated human monoclonal antibody or an
 CC antigen-binding portion, which specifically binds to human IP-10 and
 CC exhibits at least one property selected from: inhibits binding of IP-10
 CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced
 CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-
 CC react with mouse IP-10; does not cross-react with human MIG; or does not
 CC cross-react with human IFN-γ. The isolated human monoclonal antibody is
 CC useful for treating an inflammatory or autoimmune disease including
 CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease
 CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus
 CC erythematosus, Type 1 diabetes, inflammatory skin disorders (e.g.,
 CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'
 CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary
 CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,
 CC pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection,
 CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease), glaucoma,
 CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory
 CC glomerulonephritis, rapidly progressive glomerulonephritis, or
 CC atherosclerosis. It is also useful for treating a viral or bacterial
 CC infection involving unwanted IP-10 activity in a subject, where the viral
 CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present
 CC sequence represents the human IP10 monoclonal antibody heavy chain
 CC variable region DNA.
 XX
 SQ Sequence 369 BP; 76 A; 105 C; 110 G; 78 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,48e-47 Length: 369
 Score: 539.00 Matches: 101
 Percent Similarity: 89.9% Conservative: 15
 Best Local Similarity: 78.3% Mismatches: 7
 Query Match: 77.0% Indels: 6
 DB: 14 Gaps: 3
 US-10-092-640-32 (1-129) x ABB01074 (1-369)
 QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuValProGlyGlnSerLeuVal 20
 Db 1 GAGGGACACTGCTGAGTCTGAGCAGAGTAAACCCGGGAGTCTGAAAGATC 60
 QY 21 SerCysLysGlySerGlyTyrIleSerPheThrSerTyrTyrPheValAlaArgGlnMet 40
 Db 61 TCTCTGAAGAGTTTCGATACCACTTCCAGCTATGATGCGCTGGTGGCCAGATG 120
 QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuLeuTyrProGlyLysSerAspThrIleTyr 60
 Db 121 CCCGGGAAAGGCTGAGTGGATGGGCTCATCTCTCCGAGTACCTCATACCGAGATAC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 181 ACCCGCTCTTCCAGGCCCAAGTCACTACACCGCAAGTCCATCCAGCAGCTCTAC 240
 QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 Db 241 CTGAGTGGAGCAGCCTGAAGGCTCGACACCGCATGATATACGTGCGAGA----- 294

QY 101 ValGlyTyrCysSerSerPheGlnValAlaValTyrProGlyTyrPheGlnHisTyrGly 120
 Db 295 ---GGATATTGTAAGTGTGTGTACTCTC-----TACCCTA---TTCTTCCAGTACTGGGCG 342
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 Db 343 CAGGGCACCCTGTGTACCTCTCTCC 369
 RESULT 12
 ID ABB274803
 AB274803 standard; DNA; 660 BP.
 XX
 AC AB274803;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Human anti-TIMP-1 antibody heavy chain #30 DNA.
 XX
 KW Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;
 KW matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatotropic;
 KW variable light chain; cytosolic; nephrotropic; cardiac; liver fibrosis;
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer; gene; ss;
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200286085-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002WO-US012801.
 XX
 PR 24-APR-2001; 2001US-0285683P.
 XX
 PA (PARP) BAYER CORP.
 PA (MORP-) MORPHOSYS AG.
 XX
 PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
 DR WPI: 2003-129114/12.
 DR P-PSDB; ABB01532.
 XX
 PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1) antibodies,
 PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
 PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
 PT cancer.
 XX
 PS Claim 34; Page 203; 228pp; English.
 XX
 CC The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of TIMP
 CC -1. The antibody comprises a variable heavy chain (VHCDR3 region and a
 CC variable light chain (VLCDR3 region). An antibody preparation of the
 CC invention has hepatotropic, cytosolic, nephrotropic and cardiac
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
 CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
 CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
 CC fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The
 CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
 CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
 CC sequences shown in ABB274774-ABB274816 encode the heavy chain regions of a
 CC human anti-TIMP-1 antibody of the invention
 XX
 SQ Sequence 660 BP; 161 A; 164 C; 196 G; 139 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9.04e-47 Length: 660
 Score: 534.50 Matches: 99
 Percent Similarity: 86.0% Conservative: 12

KM alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KM lupus nephritis; glomerulosclerotic renal disease; lung cancer; gene; ss;
 KM idiopathic pulmonary fibrosis; benign prostatic hypertrophy; colon cancer.
 XX
 OS Homo sapiens.
 XX
 PN MO200286085-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002MO-US012801.
 XX
 PR 24-APR-2001; 2001US-0285683P.
 XX
 PA (FARB) BAYER CORP.
 PI (MORP-) MORPHOSYS AG.
 PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
 XX
 DR MPI; 2003-129114/12.
 DR P-PSDB; ABR01542.
 XX
 PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1) antibodies,
 PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
 PT is elevated, e.g. liver fibrosis, benign prostatic hypertrophy or lung
 PT cancer.
 XX
 PS Claim 34; Page 205-206; 228bp; English.
 XX
 CC The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of TIMP
 CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
 CC variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiac
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
 CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
 CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
 CC fibrosis, benign prostatic hypertrophy, lung cancer or colon cancer. The
 CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
 CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
 CC sequences shown in AB274774-AB274816 encode the heavy chain regions of a
 CC human anti-TIMP-1 antibody of the invention
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 XX
 Alignment Scores:
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 Score: 532.50 Matches: 101
 Percent Similarity: 84.8% Conservative: 11
 Best Local Similarity: 76.5% Mismatches: 5
 Query Match: 76.1% Indels: 15
 DB: 10 Gaps: 2
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 QY 21 SerCysLeuGlnGlySerGlyTyrSerPheMetSerTyrTyrIleAlaTyrValArgGlnMet 40
 Db 61 AGCTGCAAAAGGTTCCGATATTCCTTACAGCATATTGGATTGGCTGGCGCCGACAGATG 120
 QY 41 ProGlyLysGlnLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspTyrLysTyr 60
 Db 121 CTTGGGAAGGGCTTCAGAGTGGATGGAGGATTAATTAATTCGGGCAATAGCGATACCGGTAT 180
 QY 61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 181 TCTCCAGGCTTTCAGGGCCAGTGAACCATTAAGCGGATTAAGCAACCGGTAT 240

QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 Db 241 CTTCAATGAGCAGCCCTGGAAGGAGCAGATACCGGCATGATTATTCGCGCGCT----- 294
 QY 101 ValGlyTyrCysSerSerSerSerAlaValTyrProGlyLys-----TyrPheGln 117
 Db 295 -----CTTATCTGAGGATCTTATTATTGAT 324
 QY 118 HisTyrGlyGlnGlyThrLeuValThrValSerSer 129
 Db 325 TATTGGGCGCAAGCACCTCGTGACGGTTAGCTCA 360
 RESULT 15
 AB274813
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 XX
 AC AB274813;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Human anti-TIMP-1 antibody heavy chain #40 DNA.
 XX
 DE Human: antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VHC/DR3;
 KM matrix metalloproteinase; MMP; variable heavy chain; VHC/DR3; hepatotropic;
 KM variable light chain; cytostatic; nephrotropic; cardiac; liver fibrosis;
 KM alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KM lupus nephritis; glomerulosclerotic renal disease; lung cancer; gene; ss;
 KM idiopathic pulmonary fibrosis; benign prostatic hypertrophy; colon cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200286085-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002MO-US012801.
 XX
 PR 24-APR-2001; 2001US-0285683P.
 XX
 PA (FARB) BAYER CORP.
 PI (MORP-) MORPHOSYS AG.
 PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
 XX
 DR MPI; 2003-129114/12.
 DR P-PSDB; ABR01542.
 XX
 PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1) antibodies,
 PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
 PT is elevated, e.g. liver fibrosis, benign prostatic hypertrophy or lung
 PT cancer.
 XX
 PS Claim 34; Page 207; 228bp; English.
 XX
 CC The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of TIMP
 CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
 CC variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiac
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
 CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
 CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
 CC fibrosis, benign prostatic hypertrophy, lung cancer or colon cancer. The
 CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
 CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
 CC sequences shown in AB274774-AB274816 encode the heavy chain regions of a
 CC human anti-TIMP-1 antibody of the invention
 XX
 SQ Sequence 672 BP; 162 A; 164 C; 198 G; 148 T; 0 U; 0 Other;

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:28:39 ; Search time 4241.95 Seconds

(without alignments)
2550.806 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700
Sequence: 1 QVQLQSGNGLKPKGSESLK.....AKRPFYFQHWGQSTLVTVSS 129

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-OUTFMT=pco NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=adbs05h
-USER=US10092640@CGN_1_1.7986@runat.25052006.155716.5880 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_esc3: *
3: gb_esc4: *
4: gb_esc5: *
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7: gb_esc8: *
8: gb_esc9: *
9: gb_esc10: *
10: gb_esc11: *
11: gb_esc12: *
12: gb_esc13: *
13: gb_esc14: *
14: gb_esc15: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	540	77.1	658	3	BM713153
2	527.5	75.4	857	2	BM713153 UI-E-EUO-
3	526.5	75.2	843	2	BM713153 UI-E-EUO-
4	524	74.9	1114	3	BM920470

5	523.5	74.8	573	9	DA978565
6	523.5	74.8	795	2	BG685604
7	522.5	74.8	873	2	BG754454
8	522.5	74.6	536	6	DA988840
9	520	74.3	607	2	BG755575
10	516.5	73.8	568	9	DA988827
11	515.5	73.6	875	3	BQ711293
12	515	73.5	573	3	DA981607
13	514.5	73.5	530	9	DB190036
14	514.5	73.5	584	9	DA969213
15	513	73.2	476	7	BF663762
16	512.5	73.2	476	7	DB109549
17	511.5	73.1	556	9	DA954639
18	509.5	72.8	438	7	AM402496
19	509.5	72.8	921	3	BQ710635
20	506.5	72.4	487	7	AM403158
21	506.5	72.4	777	2	BG754281
22	503	71.9	511	9	DA962753
23	502.5	71.8	566	9	DA930979
24	502	71.7	565	9	DA977102
25	501	71.6	957	3	BQ709811
26	500	71.4	559	9	DA984100
27	499.5	71.4	444	7	AM401565
28	499	71.3	568	9	DB115918
29	498.5	71.2	880	3	BQ712042
30	498	71.1	511	9	DA930878
31	495	70.7	545	9	DA979866
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33	493.5	70.5	863	2	BG756025
34	492.5	70.4	652	2	BG757902
35	492.5	70.4	905	2	BG686261
36	492	70.3	754	9	DA581067
37	491.5	70.2	571	9	DA986278
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ALIGNMENTS

RESULT 1
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LOCUS 658 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-EUO-ahn-d-09-0-UI.r1 UI-E-EUO Homo sapiens cDNA clone
UI-E-EUO-ahn-d-09-0-UI 5', mRNA sequence.

ACCESSION BM713153
VERSION BM713153.1 GI:19026411
KEYWORDS EST.

SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS Bonaldo, M.P., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548

COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

Db 271 AGCCGCTCTCCAGGCGCAGTCACCATCTCAGCCGACAGTCCATCAGACCCGCTAC 330
 QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTrpPheCysAlaArgHisAsp 100
 Db 331 CTCACAGGAGCGAGCCCTGGAAGGCTCCGACACCGCCATGATTACTGTGGAGACAGAG 390
 QY 101 ValGlyTrpCysSerSerSerAanCysAlaLysTrpProGluTrpPheGlnHisTrpGly 120
 Db 391 CAGTGGCTGTGACGAGAAAGTGG-----TTCCAGACCCCTGGGCG 429
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 DEFINITION mRNA sequence.
 ACCESSION BG754240
 VERSION BG754240.1 GI:14064893
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 843)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-rc@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM1686 row: f column: 23
 High quality sequence stop: 801.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:4846102"
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 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pOT87; Site: 1: XhoI;
 Site 2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.17e-49 Length: 843
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 Query Match: 75.2% Indels: 5
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 QY 21 SerCysLysGlySerGlyTrpSerPheThrSerTrpIleAlaTrpValArgIleMet 40
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 QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTrpPheCysAlaArgHisAsp 100
 Db 299 CTCACAGGAGCGAGCCTGGAAGGCTCCGACACCGCCATGATTACTGTGGAGACAG- 355
 QY 101 ValGlyTrpCysSerSerSerAanCysAlaLysTrpProGluTrpPheGlnHisTrpGly 120
 Db 356 -----GGTAGCAGACAGCTGTACACGACAAAGAACTGTTCCACCCCTGGGCG 403
 QY 121 GlnGlyThrLeuValThrValSerSer 129
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 5', mRNA sequence.
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 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 1114)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-rc@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM12781 row: g column: 22
 High quality sequence stop: 736.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5750445"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_122"
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleens. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH_MGC Library."
 FEATURES
 source

ORIGIN

Alignment Scores:

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Percent Similarity:	84.6%	Conservative:	11
Best Local Similarity:	76.2%	Mismatches:	6
Query Match:	74.9%	Indels:	14
DB:	3	Gaps:	2

US-10-092-640-32 (1-129) x BM920470 (1-1114)

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DEFINITION DA978565 SYN0V2 Homo sapiens cDNA clone SYN0V2009762 5', mRNA
ACCESSION DA978565.1 GI:82439030
VERSION   DA978565
KEYWORDS EST.
SOURCE    Homo sapiens (human)
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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 573)
AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
          Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Makaguri,H.,
          Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
          Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
          Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
          Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
          Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
          Genome Res. 16 (1), 55-65 (2006)
JOURNAL   PUBLISHED
          16344560
COMMENT   Contact: Takao Isegai
          Fli Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatarari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: fli-cdna@fli.com
          NEDO human cDNA project (New Energy and Industrial Technology

```

FEATURES

Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

Location/Qualifiers

1..573

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="SYNOV2009762"

/tissue="synovial membrane tissue from rheumatoid arthritis"

/clone_lib="SYNOV2"

/note="Vector: pMT185FL3"

ORIGIN

Alignment Scores:

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Score:	523.50	Matches:	98
Percent Similarity:	86.0%	Conservative:	13
Best Local Similarity:	76.0%	Mismatches:	15
Query Match:	74.8%	Indels:	3
DB:	9	Gaps:	1

US-10-092-640-32 (1-129) x DA978565 (1-573)

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QY      1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuLysProGlyGlnSerLeuLysIle 20
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DB      114 GAGGTGCAGCTGTGTCAGTCTGAGCAGAGGTGAAAAACCCGGGAGTCTTGAAGATC 173

QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
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DB      174 TCCTGTAAAGGGTTCTGGATACAGCTTTACCACTACTGATCGGCTGGTGCCAGATG 233

QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
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DB      234 CCCGGGAAAGGCTGTGAGTGGATGGGATCATCTATCTGTGACTCTGTATCCAGATTC 293

QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      294 AGCCGCTCTTCCAAAGGCCAGGTCACTTCCAGCCGACACTCCATCCATCCAGCCGCTTAC 353

QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
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DB      354 CTGCAGTGGAGCAGCCTGGAAGGCTCGACACCGCATGTATTACTGTGCGAGACTACT 413

QY      101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyLysPheGlnHisTrpGly 120
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      414 CATGGTATTACTATGATGATGATGCTCTTAT-----TACTATCTTGACTACTGGGCG 464

QY      121 GlnGlyThrLeuValThrValSerSer 129
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      465 CAGGGAACCTGTGTCACTCTCTCTCA 491

RESULT 6
LOCUS   BG685604 795 bp mRNA linear EST 01-MAY-2001
DEFINITION BG685604 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765028 5', mRNA sequence.
ACCESSION BG685604
VERSION   BG685604.1 GI:13917001
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 795)
AUTHORS   NIH-MGC http://mhc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
COMMENT

```

Email: c9abps@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM623 row: d column: 21
 High quality sequence stop: 789.

FEATURES

source

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1.795
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:4765028"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
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ORIGIN

Alignment Scores:

Pred. No.:	2.38e-49	Length:	795
Score:	523.50	Matches:	98
Percent Similarity:	86.0%	Conservative:	13
Best Local Similarity:	76.0%	Mismatches:	13
Query Match:	74.8%	Indels:	5
DB:	2	Gaps:	2

US-10-092-640-32 (1-129) x BG685604 (1-795)

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QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLeuLeuProGlyGluSerLeuLeuSile 20
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DB 94 GAGGTGACACTGTGTGAGTGTGAGCAGAGGTAAAGCCCGGAGAGTCTCGAAGATC 153

QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnmet 40
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DB 154 TCTGTAAAGGTTCTGATACAGCTTATCACTACTGATCGGCTGGGCGCCAGATG 213

QY 41 ProGlyLysGlyLeuGlnLutyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
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DB 214 CCCGGGAAAGGCTGAGAGTGATGGGATCATCTATCTGCTGATCTATATACCAATAC 273

QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
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DB 274 AGCCGCTCTTCCAAAGCCAGGTCATATTATTCAGCCGACAGTCATCAGTACCGCTAC 333

QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
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DB 334 CTGCTATGAGCAGCCTGAAAGGCTCGACACCGCATATTAATGTCGAGACATGAT 393

QY 101 ValGlyTyrCysSerSerSerLeuLysValAlaLysTrpProGlyLysPheGlnHisTrpGly 120
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DB 394 ---GGTTACTATGATTCGGGGAGC-----CCGCACTACATTGACTCTCGGGAGC 438

QY 121 GlnGlyThrLeuValThrValSerSer 129
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DB 439 CAGGGAAACCTAGTACCGTCTCTCTCA 465
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RESULT 7
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 LOCUS 602710060FL NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846527 5',
 DEFINITION mRNA sequence.

ACCESSION
 VERSION BG754454.1 GI:114065094
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: c9abps@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM1687 row: h column: 16
 High quality sequence stop: 821.

FEATURES

source

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1.873
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4846527"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 48"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
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ORIGIN

Alignment Scores:

Pred. No.:	2.72e-49	Length:	873
Score:	523.50	Matches:	98
Percent Similarity:	86.0%	Conservative:	13
Best Local Similarity:	76.0%	Mismatches:	13
Query Match:	74.8%	Indels:	5
DB:	2	Gaps:	2

US-10-092-640-32 (1-129) x BG754454 (1-873)

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QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLeuLeuProGlyGluSerLeuLeuSile 20
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DB 94 GAGGTGACACTGTGTGAGTGTGAGCAGAGGTAAAGCCCGGAGAGTCTCGAAGATC 153

QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnmet 40
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 154 TCTGTAAAGGTTCTGATACAGCTTATCACTACTGATCGGCTGGGCGCCAGATG 213

QY 41 ProGlyLysGlyLeuGlnLutyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 214 CCCGGGAAAGGCTGAGAGTGATGGGATCATCTATCTGCTGATCTATATACCAATAC 273

QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
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DB 274 AGCCGCTCTTCCAAAGCCAGGTCATATTATTCAGCCGACAGTCATCAGTACCGCTAC 333

QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 334 CTGCTATGAGCAGCCTGAAAGGCTCGACACCGCATATTAATGTCGAGACATGAT 393
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QY 101 ValGIYrCySerSerSerSerSancysAlalySTrPrProGIYrYrPhedInhiSTrPGly 120
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 Db 394 ---GGTACTATGATTCGGGACC-----CCGACTACATTGACTCTCGGGGC 438
 QY 121 GInGIYrThrLeuValThrValSerSer 129
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 Db 439 CAGGAGACCCCTAGTCACCCCTCTCTCA 465

RESULT 8
 DA988840 536 bp mRNA linear EST 09-NOV-2005
 LOCUS DA988840 SYN0V3 Homo sapiens cDNA clone SYN0V3000550 5', mRNA
 DEFINITION
 sequence.
 ACCESSION DA988840 GI:81266680
 VERSION DA988840.1 GI:81266680
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 536)
 AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
 Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 TITLE Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FUJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: fli-cdna@hri.fuj.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction;
 Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing; RAB.
 FEATURES
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 /tissue_type="synovial membrane tissue from rheumatoid
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 /clone_lib="SYNOV3"
 /note="Vector: pMR18SFL3"

ORIGIN
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 Best Local Similarity: 77.0% Mismatches: 10
 Query Match: 74.6% Indels: 5
 Db: 9 Gaps: 2
 US-10-092-640-32 (1-129) x DA988840 (1-536)

QY 4 LeuLeuGIrSerGIrAlaGIrLeuValSylsPrProGIYrGIrSerLeuValSylsSerCysLys 23
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 Db 124 CTGGTGCAGCTCTGGAGCAGAGGTGAGAAAGCCCGGGAGCTCTCAAGATTCTTGTAAG 183
 QY 24 GlySerGIrYrSerSerTherSerYrTrpIleAlaTrpValArgGlnMetPrProGIYrLys 43

Db 104 GGTTCGATACAGCTTTTACACGACTCTGATCGCTGAGTGCACCAATGCCGGGAAA 243
 QY 44 GYLeuGIrYrMetGIrLeuIleYrPrProGIrYrAspSerAspThrLysYrSerProSer 63
 |||||
 Db 244 GGCCGTGAGTGATGGGATGATCATCTATCTGTGATCTGTATACCAAGATGAGCCGTC 303

QY 64 PheGIrGIrYrGlnValThrIleSerValAspLysSerValSerThrAlaYrLeuGIrTrp 83
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 Db 304 TTCGAGGCGCAGGTACCATCTACAGCCGACAGTCAATCAGTACCGCTTACCTGACGTGG 363

QY 84 SerSerLeuLysPrProSerAspSerAlaValYrPheCysAlaArgHisAspValIleYr 103
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 Db 364 AGCAGCTGAGAGCGCTCGACACGCCCATGRTTACTGTGACAGAG-----GCATT 417

QY 104 CysSerSerSerAsnCysAlaLysTrpPrProGIrYrPheGlnHisTrpGIrYrGlnGIrYr 123
 |||||
 Db 418 TGTACTAGTACCAACTGCTAT-----TCCAGCTTCGCTACTGAGGGCCAGGGAACC 468

QY 124 LeuValThrValSerSer 129
 |||||
 Db 469 CTGGTCACCGCTTCTCA 486

RESULT 9
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 LOCUS 602716258P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856390 5',
 DEFINITION
 mRNA sequence.
 ACCESSION BG755575
 VERSION BG755575.1 GI:14066228
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 607)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bcr-mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LILCM1707 row: c column: 15
 High quality sequence stop: 605.
 FEATURES
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 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming;
 directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Alignment Scores:
 Pred. No.: 4.12e-49 Length: 607

Score: 520.00
 Percent Similarity: 84.5%
 Best Local Similarity: 75.2%
 Query Match: 74.3%
 DB: 2
 Matches: 97
 Conservative: 12
 Mismatches: 10
 Indels: 10
 Gaps: 1

US-10-092-640-32 (1-129) x BG755575 (1-607)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
 DB 102 GAGGTGACGTGGTGCAGCTGTGAGCAGAGTGAAGCCGGGAGTCTCTGAAGATC 161
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
 DB 162 TCCTGTAAAGGTTCTGGATACACTTTACAGCTACGATCGGCTGGGCGCCAGATG 221
 QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
 DB 222 CCGGGAAAGCCTCGAGTGGATCGGGATCATCTATCTGTGACTGTGATACCAATAC 281
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 DB 282 AGCCCTCTCTCCAAAGGCCAGTGCACCATCTCAAGCCAGATCCATCAGACCGCCTAC 341
 QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 DB 342 CTGCACGTGAGCAGCCTCGAAGCCTCGACACCGCATGATTACTGTGGTCCCATCA 401
 QY 101 ValGlyTyrCysSerSerSerSerSerValAlaLysTyrProGlyLysPheGlnHisTyrGly 120
 DB 402 ACAGGCTCTGCTCTCT-----TTTGATATCTGGGGC 411
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 DB 432 CAAGGACAATGGTCAACGCTCTCTCA 458

RESULT 10

DA988827 568 bp mRNA linear EST 09-NOV-2005
 LOCUS DA988827 SYN0V3 Homo sapiens cDNA clone SYN0V3000537 5', mRNA
 DEFINITION sequence.

ACCESSION DA988827
 VERSION DA988827.1 GI:81266627
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 568)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Oca, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsutsumi, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Rie, R., Kuehida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Magatsuna, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T., and Sugano, S.
 Diverisification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

JOURNAL PUBMED COMMENT

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 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one

FEATURES
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 pass sequencing: RAB.
 Location/Qualifiers
 1..568
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SYNOV3000537"
 /tissue_type="synovial membrane tissue from rheumatoid arthritis"
 /clone_lib="SYNOV3"
 /note="Vector: pME18SFLJ3"

ORIGIN

Alignment Scores:
 Pred. No.: 9,49e-49 Length: 568
 Score: 516.50 Matches: 98
 Percent Similarity: 84.5% Conservative: 11
 Best Local Similarity: 76.0% Mismatches: 13
 Query Match: 73.8% Indels: 7
 DB: 9 Gaps: 2

US-10-092-640-32 (1-129) x DA988827 (1-568)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
 DB 115 GAGGTGACGTGGTGCAGCTGTGAGCAGAGTGAAGCCGGGAGTCTCTGAAGATC 174
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
 DB 175 TCCTGTAAAGGTTCTGGATACACTTTACAGCTACGATCGGCTGGGCGCCAGATG 234
 QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
 DB 235 CCGGGAAAGCCTCGAGTGGATCGGGATCATCTATCTGTGACTGTGATACCAATAC 294
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 DB 295 AGCCCTCTCTCCAAAGGCCAGTGCACCATCTCAAGCCAGATCCATCAGACCGCCTAC 354
 QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 DB 355 CTGCACGTGAGCAGCCTCGAAGCCTCGACACCGCATGATTACTGTGGAGACCGGGC 414
 QY 101 ValGlyTyrCysSerSerSerSerSerValAlaLysTyrProGlyLysPheGlnHisTyrGly 120
 DB 415 GCGAGCTAC-----TACCCGTGGGCTCT---TTTGATATCTGGGGC 453
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 DB 454 CAAGGACAATGGTCAACGCTCTCTCA 480

RESULT 11

BO711293 875 bp mRNA linear EST 16-JUN-2002
 LOCUS AGENCOURT_8349985 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280207
 DEFINITION 5', mRNA sequence.

ACCESSION BO711293
 VERSION BO711293.1 GI:21850192
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 875)
 AUTHORS NIH-MGC http://img.ncbi.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM2471 row: a column: 08
 High quality sequence stop: 594.

FEATURES

source

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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 113"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	2,27e-48	Length:	875
Score:	515.50	Matches:	97
Percent Similarity:	85.3%	Conservative:	13
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Query Match:	73.6%	Indels:	7
DB:	3	Gaps:	1

US-10-092-640-32 (1-129) x B0711293 (1-875)

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QY      1  GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
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QY      21  SerCylsGlySerGlyTyrSerPheThrSerTyrTrrIleAlaTrpValArgGlnMet 40
       |||||||
DB      145  TCCTGTAAAGGTTCTGGATACAGTTTACAGTACATGATCGCGGTGGCGCAGATG 204

QY      41  ProGlyLysGlyLeuGlnLutyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
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DB      205  CCCGGGAAAGCCCTGGAGTGGATGGGATCATCTATCTCGGACTCTATACGACATTC 264

QY      61  SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
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DB      265  AGCCCGTCTCTTCCAAGGCCAGGTACCATCTCAGTCGACCAAGTCCATCAATACCGCTAC 324

QY      81  LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
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DB      335  CTGGAGTGGCGCAGTCTGAAGGCTCTGACACCGCATATATTATGTGCGAGACAT--- 381

QY      101  ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyLutyrPheGlnHisTrpGly 120
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QY      121  GlnGlyThrLeuValThrValSerSer 129
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DB      424  CAGGAAACCTGTGTCACGCTCTCTCA 450

RESULT 12
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LOCUS     DA981607  SYN02  Homo sapiens cDNA clone SYN02013648 5', mRNA
DEFINITION
sequence.
ACCESSION DA981607
VERSION   DA981607.1  GI:82344094
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 573)

AUTHORS

Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Teuriltan,K., Wakaguri,H.,
 Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Magatsuma,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

TITLE

JOURNAL

1634560

COMMENT

Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@hri.co.jp
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.
 Location/Qualifiers

FEATURES

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 /note="Vector: pME18SFL3"

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Query Match:	73.6% <td>Indels:</td> <td>10</td>	Indels:	10
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US-10-092-640-32 (1-129) x DA981607 (1-573)

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       |||||||
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DB      356  CTGGAGTGGCGCAGCTGAAGGCTCTGACACCGCATATATTATGTGCGAGATCGACA 415

QY      101  ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyLutyrPheGlnHisTrpGly 120
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DB      416  GATGGCTACAGTATGAG-----GACTACTGGGCG 445

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QY 121 GlnGlyThrLeuValThrValSerSer 129
 DB 446 CAGGGAACCTGATCACCCTCTCTCA 472

RESULT 13
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 DEFINITION DB190036 TLUNG2 Homo sapiens cdna clone TLUNG2000849 5', mRNA

ACCESSION DB190036
 VERSION DB190036.1 GI:83552147
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

TITLE
 JOURNAL PUBLISHED
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

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 Query Match: 73.5% Indels: 7
 DB: 9 Gaps: 3

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QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg---His 99
 DB 356 CTGCAGTGAGATGAGCTCTGGAGCGGACGCCATGTATTACTGTGGACACTTCA 415

QY 100 AspValGlyTyrCysSerSerSerAanCysAlaLysTrpProGluTyrPheGlnHisTrp 119
 DB 416 TCCTTAGCGTATGCAACAC-----TGG---TACTTCTTTGACTACTGG 457

QY 120 GlyGlnGlyThrLeuValThrValSerSer 129
 DB 458 GGCAGGGAACCTGATCACCCTCTCTCA 487

RESULT 14
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 DEFINITION DA969213 STOMA2 Homo sapiens cdna clone STOMA2008143 5', mRNA

ACCESSION DA969213
 VERSION DA969213.1 GI:82348271
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

TITLE
 JOURNAL PUBLISHED
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
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 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

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 Best Local Similarity: 76.2% Mismatches: 15
 Query Match: 73.5% Indels: 3

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Oy	21	SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleLeuAlaTrpValArgGlnMet	40
Db	165	TCCTGTAAAGGAGCTCTGGATTCAAGTTTAAACAGCAACCGGATCGTCTGGGTCCGCAAGTGG	224
Oy	41	ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr	60
Db	225	CCCCGGAAAGGCGCTGGAATATATGGGACCAATCTATCTGTGATCTGTGATACCAAGAT	284
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Db	285	AACCGGTATTCACAGGCGAGGTACACATTCACAGTCGACAAATCCATCACACCGCCTAT	344
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Db	345	CTACAGTGAACACAGCTTGAAGGCTCGGACACCGCCGCTTATTTACTGTGGCGGATTAGAG	404
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Oy	120	GlyGlnGlyThrLeuValThrValSerSer	129
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ACCESSION	BF663762		mRNA sequence.
VERSION	BF663762.1	GI:11937657	
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ORGANISM	Homo sapiens		
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
	1 (bases 1 to 862)		
	NIH-MGC http://mgs.nci.nih.gov/ .		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
REFERENCE	Contact: Robert Strausberg, Ph.D.		
AUTHORS	Email: cgabs-r@mail.nih.gov		
TITLE	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
JOURNAL	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
COMMENT	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		
	Plate: Ilcm181 row: d column: 23		
	High quality sequence stop: 715.		
FEATURES	Location/Qualifiers		
SOURCE	1..862		

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Alignment Scores:			
Pred. No.:	4..31e-48	Length:	862
Score:	513.00	Matches:	100
Percent Similarity:	86.2%	Conservative:	12
Best Local Similarity:	76.9%	Mismatches:	12
Query Match:	73.3%	Indels:	7
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DB	330 CTCGAGTGGAGCAGCCTCGAAGGACCTTCGACACCGCCAGTATTACTGTGCCAGACGGGT	388	
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DB	390 CACACTGGGGATTTGTAGTGGTGGAGTGC-----TACGAGGCTACTGG	434	
QY	120 GlyGlnGlyThrLeuValThrValSerSer	129	
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Job time : 4245.95 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 17:06:37 ; Search time 167.7 Seconds
(without alignments)
2158.972 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700
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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	700	100.0	774	3	US-09-315-574-4
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4	520	74.3	462	3	US-08-758-417A-207
5	510.5	72.9	361	3	US-09-025-769B-66
6	510.5	72.9	361	3	US-09-490-070A-66
7	510.5	72.9	361	3	US-09-490-153-66
8	510.5	72.9	361	3	US-09-490-324-66

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10	500	71.4	414	3	US-08-758-417A-201	Sequence 201, App
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12	483	69.0	700	3	US-08-545-809A-51	Sequence 51, App1
13	483	69.0	700	3	US-09-515-697-51	Sequence 51, App1
14	465.5	66.5	383	2	US-08-053-131-176	Sequence 176, App
15	465.5	66.5	383	2	US-08-096-162-176	Sequence 176, App
16	460.5	65.8	357	2	US-08-053-131-156	Sequence 156, App
17	460.5	65.8	357	2	US-08-096-762-156	Sequence 156, App
18	460.5	65.8	351	2	US-08-053-131-177	Sequence 177, App
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22	459.5	65.6	417	3	US-09-505-243-39	Sequence 39, App1
23	458	65.4	348	2	US-08-053-131-157	Sequence 157, App
24	458	65.4	348	2	US-08-096-762-157	Sequence 157, App
25	457	65.3	326	2	US-08-053-131-167	Sequence 167, App
26	457	65.3	326	2	US-08-096-762-167	Sequence 167, App
27	457	65.3	366	2	US-08-053-131-163	Sequence 163, App
28	457	65.3	366	2	US-08-096-762-163	Sequence 163, App
29	457	65.3	477	3	US-08-724-752-16	Sequence 16, App1
30	457	65.3	477	3	US-09-614-092A-16	Sequence 16, App1
31	454	64.9	348	2	US-08-053-131-160	Sequence 160, App
32	454	64.9	348	2	US-08-096-762-160	Sequence 160, App
33	452	64.6	358	2	US-08-053-131-172	Sequence 172, App
34	452	64.6	358	2	US-08-096-762-172	Sequence 172, App
35	452	64.6	360	2	US-08-053-131-161	Sequence 161, App
36	452	64.6	360	2	US-08-096-762-161	Sequence 161, App
37	451	64.4	349	2	US-08-053-131-165	Sequence 165, App
38	451	64.4	349	2	US-08-096-762-165	Sequence 165, App
39	450.5	64.4	384	2	US-08-053-131-168	Sequence 168, App
40	450.5	64.4	384	2	US-08-096-762-168	Sequence 168, App
41	450	64.3	297	3	US-09-042-353-91	Sequence 91, App1
42	450	64.3	297	3	US-08-758-417A-355	Sequence 355, App
43	448.5	64.1	312	3	US-09-042-353-123	Sequence 123, App
44	448.5	64.1	312	3	US-08-758-417A-387	Sequence 387, App
45	448.5	64.1	325	2	US-08-053-131-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-08-665-202-4
Sequence 4, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0. Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..774
OTHER INFORMATION:
OTHER INFORMATION: /note="sequence of C6 sFv"
US-08-665-202-4
antibody C6.5"

Alignment Scores:
Pred. No.: 3,52e-75 Length: 774
Score: 700.00 Matches: 129
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-092-640-32 (1-129) x US-08-665-202-4 (1-774)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
DB 1 CAGGGTCACCTGTTGACAGTCTGGGGCAGAGTTGAAAAAACCAGGAGCTCTGAAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
DB 61 TCTGTGAAGGTTCTGGATACAGCTTTACAGCTACTGGATGCGCCGGGTGGCCGAGATG 120
QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuLleTyrProGlyLysSerAspThrLysTyr 60
DB 121 CCGGGGAAAGCCCTGGAGTACATGGGGCTCATCTATCTCCGTGACTCTGACACCAATATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerAlaSerThrAlaTyr 80
DB 181 ACCCGCTCTTCCAAAGCCAGGTCACCACTTCAGTGAACAAGTCCGTCCGACCTGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 TTGCAATGAGACAGCTCTGAAGCCCTCGACAGCGCCGTGATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyrPheGlnHisTrpGly 120
DB 301 GGGGATATTGCAAGTATTCACATCCGCAAGTGGCTGAATACTTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGCACCTGTGTCACCGTCTCTCTCA 387

RESULT 2
US-09-315-574-4
Sequence 4, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hene P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..774
OTHER INFORMATION:
OTHER INFORMATION: /note="sequence of C6 sFv"
US-09-315-574-4
antibody C6.5"

Alignment Scores:
Pred. No.: 3,52e-75 Length: 774
Score: 700.00 Matches: 129
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-32 (1-129) x US-09-315-574-4 (1-774)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
DB 1 CAGGTGACAGCTGTTCAAGTCTGGGGCAGAGTTGAAAAAACCAGGAGCTCTGAAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
DB 61 TCTGTGAAGGTTCTGGATACAGCTTTACAGCTACTGGATGCGCCGGGTGGCCGAGATG 120
QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuLleTyrProGlyLysSerAspThrLysTyr 60
DB 121 CCGGGGAAAGCCCTGGAGTACATGGGGCTCATCTCCGTGACTCTGACACCAATATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerAlaSerThrAlaTyr 80
DB 181 ACCCGCTCTTCCAAAGCCAGGTCACCACTTCAGTGAACAAGTCCGTCCGACCTGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 TTGCAATGAGACAGTCTGAAGCCCTCGACAGCGCCGTGATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyrPheGlnHisTrpGly 120

Db 301 GTGGATATTGCACTAGTTCACACTGCGCAAGGCGCTGATTAATCTTCAGCATGGGCG 360
QY 121 GlnGlyThrIeuValThrValSerSer 129
Db 361 CAGGGACCCCTGGTGCACCGTCTCTCA 387

RESULT 3
US-09-042-353-359
Sequence 359, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: NO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-359

Alignment Scores:
Pred. No.: 9.8e-54 Length: 462
Score: 520.00 Matches: 97
Percent Similarity: 83.7% Conservative: 11
Best Local Similarity: 75.2% Mismatches: 9
Query Match: 74.3% Indels: 12
DB: 3 Gaps: 1

US-10-092-640-32 (1-129) x US-09-042-353-359 (1-462)

QY 1 GlnValGlnIeuIeuGlnSerGlyValGluIeuLysProGlyGluSerLeuLysIle 20
Db 58 GAGTGCAGCTGCTGAGCTGAGCAGAGTAAAGCCCGGAGTCTTGAAGATC 117
QY 21 SerCysLysGlySerGlyTyrSerPheThrIleAlaTyrValArgGlnMet 40
Db 118 TCCTGTAAGGTTCTGATACAGCTTACCGGCTACGTGATCGCGTGGCGCCAGATG 177
QY 41 ProGlyLysGlyIeuGlnLysMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
Db 178 CCGGGAAAGGCGCTGAGTGGATGGGATCATCTTACCTGTGACTCTATACCAATAC 237
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 238 AGCCGCTCTTCCAGGCCAGGTACCATCTACGCCGACAGTCCATCAGACCGCCTAC 237
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 298 CTGCACTGAGCAGCTGAAAGGCGCTGACACCGCATATATCTGTGGAGAGACAA 357
QY 101 ValGlyTyrCysSerSerSerSerSerCysAlaLysTyrProGlyLysPheGlnHisTyrGly 120
Db 358 CTGGGC-----CTCTTGTACTATCGGGC 381

QY 121 GlnGlyThrIeuValThrValSerSer 129
Db 382 CAGGGACCCCTGGTGCACCGTCTCTCA 408

RESULT 4
US-08-758-417A-207
Sequence 207, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESSES:

```
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 207:
US-08-758-417A-207

Alignment Scores:
Pred. No.: 520.00 Length: 462
Score: 9.8e-54 Matches: 97
Percent Similarity: 83.7% Conservative: 11
Best Local Similarity: 75.2% Mismatches: 9
Query Match: 74.3% Indels: 12
DB: 3 Gaps: 1

US-10-092-640-32 (1-129) x US-08-758-417A-207 (1-462)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 20
Db 58 GAGGTGCAAGCTGCTGAGTCTGAGCAGAGTGAAAGCCCGGGGAGTCTGTGAAGATC 117
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaAlaTrpValArgGlnMet 40
Db 118 TCCTGTAAAGGGTTCGTGATACAGCTTACCGGCTACTGATCGGCTGGGTGGCCAGATG 177
QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
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Db 178 CCGGGAAAGCGCTGAGATGAGTGGGATCATCTCTCTGAGTACTGTATCACAATAC 237
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 238 AGCCCGTCTCTTCCAGAGCCAGAGTCCATCTCAGCCGACAGTCCATCAGCCGCCCTAC 297
QY 81 LeuGlnTyrPseSerLeuLysPseSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 298 CTGACGTGAGCAGCCTGAGCCTCGACACCGCCATGATTACTGTGCGAGAACCA 357
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
Db 358 CTGGCC-----CTTTGACTACTGGGCG 381
QY 121 GlnGlyThrLeuValThrValSerSer 129
Db 382 CAGGAAACCTGGTCCACGTCCTCTCA 408

RESULT 5
US-09-025-769B-66
Sequence 66, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic gene"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..360
OTHER INFORMATION: /product= "VHS"
US-09-025-769B-66

Alignment Scores:
Pred. No.: 9.75e-53 Length: 361
Score: 510.50 Matches: 98
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Percent Similarity: 83.2% Conservative: 11
 Best Local Similarity: 74.8% Mismatches: 9
 Query Match: 72.9% Indels: 13
 DB: 3 Gaps: 2

US-10-092-640-32 (1-129) x US-09-025-7696-66 (1-361)

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DB      1 GAAGTCAATTGGTTTCAGACGGCGCGGAGTGAATAAAACCGGCGGAAACCTGAAATTT 60
QY      21 SerCysLeuGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValaGlnMet 40
DB      61 AGCTGCAAAAGGTTCCCGATATTCCTTTACGAGCTATTGGATTGGCTGGGTCGCGCATG 120
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
DB      121 CTGGGAAAGGTTCTCGAGTGGATGGGCAATTATTATCCGGCGCATAGCCGATTAT 180
QY      61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB      181 TCTCCAGCTTTTCAGGCGCAGGTGACCATTAAGCCGATTAAGCATTAACCGCGTAT 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg----- 98
DB      241 CTTCAATGAGACGCTCGAAAGCGAGCATACGCCCATGTATTATTCGCGCGTTGGGCGC 300
QY      99 HisAspValGlyTyrCysSerSerSerAsnCyAlaLysTrpProGlyTyrPheGlnHis 118
DB      301 GGGGATGGCTTTATATCG-----ATGGAATTAT 327
QY      119 TrpGlyGlnGlyThrLeuValThrValSerSer 129
DB      328 TGGGGCCAAGGCAACCTGTGTGACGTTAGCTCA 360

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RESULT 6

US-09-490-070A-66
 Sequence 66, Application US/09490070A
 Patent No. 6696248

GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
 White & McAnuliffe
 STREET: 1666 K Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,070A
 FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37629-0005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020
 INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:
 LENGTH: 361 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "synthetic gene"

FEATURE:

NAME/KEY: CDS
 LOCATION: 1..360
 OTHER INFORMATION: /product= "vhs"
 SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
9	75e-53	361	98
Percent Similarity:	83.2%	Conservative:	11
Best Local Similarity:	74.8%	Mismatches:	13
Query Match:	72.9%	Indels:	2
DB:	3	Gaps:	2

US-10-092-640-32 (1-129) x US-09-490-070A-66 (1-361)

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QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGluSerLeuLysIle 20
DB      1 GAAGTCAATTGGTTTCAGACGGCGCGGAGTGAATAAAACCGGCGGAAACCTGAAATTT 60
QY      21 SerCysLeuGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValaGlnMet 40
DB      61 AGCTGCAAAAGGTTCCCGATATTCCTTTACGAGCTATTGGATTGGCTGGGTCGCGCATG 120
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
DB      121 CTGGGAAAGGTTCTCGAGTGGATGGGCAATTATTATCCGGCGCATAGCCGATTAT 180
QY      61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB      181 TCTCCAGCTTTTCAGGCGCAGGTGACCATTAAGCCGATTAAGCATTAACCGCGTAT 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg----- 98
DB      241 CTTCAATGAGACGCTCGAAAGCGAGCATACGCCCATGTATTATTCGCGCGTTGGGCGC 300
QY      99 HisAspValGlyTyrCysSerSerSerAsnCyAlaLysTrpProGlyTyrPheGlnHis 118
DB      301 GGGGATGGCTTTATATCG-----ATGGAATTAT 327
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DB      328 TGGGGCCAAGGCAACCTGTGTGACGTTAGCTCA 360

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RESULT 7

US-09-490-153-66
 Sequence 66, Application US/09490153
 Patent No. 6706484

GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

```

      ZIP: 10021
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/490,153
      FILING DATE: 24-Jan-2000
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/09/025,769B
      FILING DATE: 18-FEB-1998
      APPLICATION NUMBER: EP 95 11 3021.0
      FILING DATE: 18-AUG-1995
      ATTORNEY/AGENT INFORMATION:
      NAME: James F. Haley, Jr., Esq.
      REGISTRATION NUMBER: 27,794
      REFERENCE/DOCKET NUMBER: MORPHO/5
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212)596-9000
      TELEFAX: (212)596-9090
      INFORMATION FOR SEQ ID NO: 66:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 361 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
      DESCRIPTION: /desc = "synthetic gene"
      FEATURE:
      NAME/KEY: CDS
      LOCATION: 1..360
      OTHER INFORMATION: /product= "VH5"
      SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-490-153-66

Alignment Scores:
Pred. No.:          9,75e-53      Length:          361
Score:             510.50         Matches:          98
Percent Similarity: 83.2%         Conservative:     11
Best Local Similarity: 74.8%      Mismatches:       9
Query Match:       72.9%          Indels:           13
DB:                3              Gaps:             2

US-10-092-640-32 (1-129) x US-09-490-153-66 (1-361)
QY      1  GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGlnSerLeuLysIle 20
      ::::::::::::::::::::
Db      1  GAAGTGCATTGCTTCAGACGCGCGGCGAAGTGAACCAACCGGCGCAAGCCTGAAATTT 60
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
      ::::::::::::::::::::
Db      61 AGCTGCAAAAGTTCCGGATATTCTTTACGAGCTATTGGATTGGCTGGGTGGCCGAGATG 120
QY      41 ProGlyLysGlyLeuGlnTyrTyrMetGlyLeuIleTyrProGlyAspSerAspThrIleTyr 60
      ::::::::::::::::::::
Db      121 CCTGGGAAGGCTCTCGAAGTGCATTTATTATCCGCGGAGATGCGATCCGCTTAT 180
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
      ::::::::::::::::::::
Db      181 TCTCCGAGCTTTCAGGCGCAGGTGACCATTTACGCGGATMAAAGCATTTAGCACCGCGTAT 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg----- 98
      ::::::::::::::::::::
Db      241 CTTCAATGAGAGCCTGAAAGCGAGCGATACGCCCATATTATTATTCGCGGTGGGGC 300
QY      99 HisAspValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyrPheGlnHis 118
      ::::::::::::::::::::
Db      301 GCGCATGCGTTTATTCG-----ATGATTAT 327
QY      119 TrpGlyGlnGlyThrIleValThrValSerSer 129
      ::::::::::::::::::::
Db      328 TGGGGCGCAAGGACCCCTGGTGAAGGTTTACCTCA 360

```

```

RESULT 8
US-09-490-324-66
; Sequence 66, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic gene"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..360
; OTHER INFORMATION: /product= "VH5"
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-490-324-66

Alignment Scores:
Pred. No.:          9,75e-53      Length:          361
Score:             510.50         Matches:          98
Percent Similarity: 83.2%         Conservative:     11
Best Local Similarity: 74.8%      Mismatches:       9
Query Match:       72.9%          Indels:           13
DB:                3              Gaps:             2

US-10-092-640-32 (1-129) x US-09-490-324-66 (1-361)
QY      1  GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGlnSerLeuLysIle 20
      ::::::::::::::::::::
Db      1  GAAGTGCATTGCTTCAGACGCGCGGCGAAGTGAACCAACCGGCGCAAGCCTGAAATTT 60
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
      ::::::::::::::::::::
Db      61 AGCTGCAAAAGTTCCGGATATTCTTTACGAGCTATTGGATTGGCTGGGTGGCCGAGATG 120

```


QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
 Db 121 CCGGGAAGGGTCTCCAGTGAGTGGCCATTATTATCCGGGCATGCGTACCCTGTAT 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 181 TCTCCAGCTTTAAGGCGCCAGGTGACCATTAAGCGGATTAAGACATTACACCGGTAT 240
 QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg----- 98
 Db 241 CTTCAATGAGCAGCCTGAAAGCAGCATACGCGCATGATATTATGCGCGCTTGAGGCG 300
 QY 99 HisAspValGlyTyrCysSerSerSerAsnGlyAlaLysTyrProGluTyrPheGlnHis 118
 Db 301 GCGGAATGCGCTTTATTCG-----ATGATTTAT 327
 QY 119 TrpGlyGlnGlyThrLeuValThrValSerSer 129
 Db 328 TGGGGCCAAAGCACCTGTGTGACGTTAGCTCA 360
 RESULT 9
 US-09-042-353-353
 Sequence 353, Application US/09042353
 Patent No. 6255456
 GENERAL INFORMATION:
 APPLICANT: Lomborg, Nils
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 421
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042,353
 FILING DATE: 13-MAR-1998
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/853,408
 FILING DATE: 18-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/904,068
 FILING DATE: 23-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,860
 FILING DATE: 16-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/053,131
 FILING DATE: 26-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/096,762
 FILING DATE: 22-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/155,301
 FILING DATE: 18-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/161,739
 FILING DATE: 03-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/165,699

FILING DATE: 10-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/209,741
 FILING DATE: 09-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/352,322
 FILING DATE: 07-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/544,404
 FILING DATE: 10-OCT-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/728,463
 FILING DATE: 10-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US96/16433
 FILING DATE: 10-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/758,417
 FILING DATE: 02-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/21803
 FILING DATE: 01-DEC-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 014643-009040US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 353:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 414 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-042-353-353
 Alignment Scores:
 Pred. No.: 2.2e-51 Length: 414
 Score: 500.00 Matches: 94
 Percent Similarity: 84.1% Conservative: 12
 Best Local Similarity: 74.6% Mismatches: 10
 Query Match: 71.4% Indels: 10
 DB: 3 Gaps: 1
 US-10-092-640-32 (1-129) x US-09-042-353-353 (1-414)
 QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyLysSerLeuLysIle 20
 Db 67 GAGGTGACCTGTGATGAGTCTGAGCAGAGGTAAGAAAGCCGGGAGTCTTGAAGATC 126
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
 Db 127 TCTGTAAAGGCTTCGATACAGCTTTACCACTTACGATGCGCTGGATGCCCGAGATC 186
 QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
 Db 187 CCGGGAAGGGCTCGAGTGGATGGGATCATCGATCTGACTGATACCAAGATAC 246
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 247 AACCGCTCTTCCAAAGGCCAGGTGACCATCTCAGCCGACAAGTCCATGATCCGCTAT 306
 QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 Db 307 TTGCAATGAGCAGCCTGAAAGCAGCATACGCGCATGATATTACTGTCCGAGACA--- 363
 QY 101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTyrProGluTyrPheGlnHisTrpGly 120
 Db 364 -----GCGAAGTGAAGTGTACTTCTCTCTGAGGCG 396
 QY 121 GlnGlyThrLeuValThr 126

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Db          397  CGTGGACCTGCTACT  414
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RESULT 10
US-08-758-417A-201
: Sequence 201, Application US/08758417A
: Patent No. 6100129
GENERAL INFORMATION:
APPLICANT: Lomberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,111
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 201:
US-08-758-417A-201

Alignment Scores:
Pred. No.: 2,2e-51 Length: 414
Score: 500.00 Matches: 94
Percent Similarity: 84.1% Conservative: 12
Best Local Similarity: 74.6% Mismatches: 10
Query Match: 71.4% Indels: 10

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DB:	3	Gaps:	1
US-10-092-640-32 (1-129) x US-08-758-417A-201 (1-414)			
QY	1 GlnValGlnLeuLeuInserGlyValGlnLeuLeuLysProGlyGlnSerLeuLysIle 20		
Db	67 GAGGTGACGCTGGTGCAGTCTGGACAGAGGAGGAAAAAGCCCGGGAGTCTTGAGATC 126		
QY	21 SerCysAlaGlySerGlyTyrSerPheThrSertyrTrpIleAlaTrpValArgGlnMet 40		
Db	127 TCGTGAAGGGTTCTGATACAGCTTTACCCAGTTACTGATGAGCGCTGGGTGCCAATG 186		
QY	41 ProGlyLysGlyLeuGlnTyrMetCylLeuLeuIleTyrProGlyLysPheSerPheThrLysTyr 60		
Db	187 CCGGAGAAAGGCTGGAGTGGAGGAGATCATGATCTGCTGACTGTGATACCAAGATAC 246		
QY	61 SerProSerPheGlnGlyValThrIleSerValAspLysSerValSerThrAlaTyr 80		
Db	247 AACCCGCTCTTCCAAAGCCAGGTGCACATCTTCAGCCGACAGATCATCAGTACCGCTAT 306		
QY	81 LeuGlnTrpSerSerLeuLysProSerLysPheSerAlaValTyrPheCysAlaArgHisAsp 100		
Db	307 TTCAGATGAGCAGCCTGAAAGCCTCGGACCCGCAATGATTTACTGTGCCAGACA-- 363		
QY	101 ValGlyTyrCysSerSerSerAsnCySAAlaLysTrpProGlyTyrPheGlnHisTrpGly 120		
Db	364 -----GGAACAGTGAACAGTGTGACTTGTTCTGTGGGC 396		
QY	121 GlnGlyThrLeuValThr 126		
Db	397 CCGGACACCTGTGCTACT 414		
RESULT 11			
US-09-905-243-6			
/ Sequence 6, Application US/09905243			
/ Patent No. 6936698			
/ GENERAL INFORMATION:			
/ APPLICANT: Taylor, Alexander H			
/ TITLE OF INVENTION: Monoclonal Antibodies with Reduced			
/ TITLE OF INVENTION: Immunogenicity			
/ FILE REFERENCE: P50770			
/ CURRENT APPLICATION NUMBER: US/09/905,243			
/ CURRENT FILING DATE: 2001-07-16			
/ PRIOR APPLICATION NUMBER: 09/300,970			
/ PRIOR FILING DATE: 1999-04-28			
/ NUMBER OF SEQ ID NOS: 97			
/ SOFTWARE: FastSeq for Windows Version 3.0			
/ SEQ ID NO 6			
/ LENGTH: 421			
/ TYPE: DNA			
/ ORGANISM: Pan troglodytes			
/ FEATURE:			
/ NAME/KEY: CDS			
/ LOCATION: (1)...(421)			
US-09-905-243-6			
Alignment Scores:			
Prod. No.:	1,11e-49	Length:	421
Score:	486.00	Matches:	92
Percent Similarity:	80.8%	Conservative:	13
Best local Similarity:	70.8%	Mismatches:	13
Query Match:	69.4%	Indels:	12
DB:	3	Gaps:	2
US-10-092-640-32 (1-129) x US-09-905-243-6 (1-421)			
QY	1 GlnValGlnLeuLeuInserGlyValGlnLeuLysProGlyGlnSerLeuLysIle 20		
Db	61 GAGGTGACGCTGGTGCAGTCTGGACAGAGGAGGAAAAAGCCCGGGAGTCTTGAGATC 120		
QY	21 SerCysAlaGlySerGlyTyrSerPheThrSertyrTrpIleAlaTrpValArgGlnMet 40		
Db	121 TCGTGAAGGGTTCTGATACAGCTTTTACCAATCTGATGAGCGCTGGGTGCCAATG 180		

```

QY 41 ProGlyLyseGlyLeuGlyTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db 181 CCGGGGAAAGCCCGGAGTGCATGGGGATCATCTATCTGATCTGATACCATATC 240
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 241 AGCCCTCTCTCCAAAGGCCAGTCCATCTCAGCCGACAGTCCATCAGCCGCTAC 300
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 301 CTCAATAGGAGCAACTGGAAGCCTCGGACACCGCATATATATCTGTGGAG- 354
QY 101 ValGlyTyrCysSerSerSerSerSerValAlaLysTyrPro-----GlyTyrPheGlnHis 118
Db 355 -----TGTTATGCTTGACCTACTTGCAAGCTTTGATATC 390
QY 119 TyrGlyGlnGlyThrLeuValThrValSer 128
Db 391 TGGGGCCAAAGGCAATGTCACCGTCTCT 420

RESULT 12
US-08-545-809A-51
; Sequence 51, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
; US-08-545-809A-51

Alignment Scores:
Pred. No.: 5,22e-49 Length: 700
Score: 483.00 Matches: 87

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Percent Similarity: 96.0% Conservative: 10
Best Local Similarity: 86.1% Mismatches: 4
Query Match: 69.0% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-32 (1-129) x US-08-545-809A-51 (1-700)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
Db 308 GAGGTCCAGCTGTGTCAGTGTGAGCAGAGGTGAAAAAGCCCGGAGTCTCGAAGATC 367
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrThrIleAlaTyrValaGlnMet 40
Db 368 TCTGTGAAGGTTCTGATACACCTTACCGACTGATCGGCTGGGTGCCAGATG 427
QY 41 ProGlyLyseGlyLeuGlyTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db 428 CCGGGGAAAGCCCTGAGAGTGGATGGGATCATCTATCTGTGATCTGATACCATATC 487
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 488 AGCCCTCTCTCCAAAGGCCAGTCCATCTCAGCCGACAGTCCATCAGCCGCTAC 547
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 548 CTGAGTGGAGAGCCTGGAAGCCTCGGACACCGCATATATATCTGTGGAGACACACA 607
QY 101 Val 101
Db 608 GTG 610

RESULT 13
US-09-515-697-51
; Sequence 51, Application US/09515697
; Patent No. 6936705
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,697
; FILING DATE: 29-FEB-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809
; FILING DATE: 27-MAR-1996
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 base pairs
; TYPE: nucleic acid

```

```
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: GM1
SEQUENCE DESCRIPTION: SEQ ID NO: 51
US-09-515-697-51

Alignment Scores:
Pred. No.: 5,22e-49 Length: 700
Score: 483.00 Matches: 87
Percent Similarity: 96.0% Conservative: 10
Best Local Similarity: 86.1% Mismatches: 4
Query Match: 69.0% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-32 (1-129) x US-09-515-697-51 (1-700)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGlnSerLeuLysIle 20
   |||
Db 308 GAGGTGCACCTGCTGAGCTGTGAGCAGAGTGAAGCCCGGAGCTCTGAAAGATC 367

QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
   |||
Db 368 TCTGTAGGGTTTGTGATACAGCTTTACAGCTGATCGGCTGGGTCGCCAGATG 427

QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
   |||
Db 428 CCCGGAAAGCCCTGGAGTGGATGGGATCATCTATCTGTGACTGTGATACAGATG 487

QY 61 SerProSerPheGlnGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
   |||
Db 488 AACCCCTCTTCCAAAGCCAGGTCACCATCTCAGCCGACAAAGTCATCCAGCACCGCTAC 547

QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
   |||
Db 548 CTGCATGAGACGACCTGAAGGCTCGGACACCCGATGTTACTGTGCGAGACACACA 607

QY 101 Val 101
   |||
Db 608 GTG 610

RESULT 14
US-08-053-131-176
; Sequence 176, Application US/08053131
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-Apr-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-Dec-1992
```

```
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-Dec-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2422
; TELEFAX: 415-326-2400
; INFORMATION FOR SEQ ID NO: 176:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-053-131-176

Alignment Scores:
Pred. No.: 2,92e-47 Length: 383
Score: 465.50 Matches: 88
Percent Similarity: 85.0% Conservative: 8
Best Local Similarity: 77.9% Mismatches: 12
Query Match: 66.5% Indels: 5
DB: 2 Gaps: 2

US-10-092-640-32 (1-129) x US-08-053-131-176 (1-383)

QY 17 SerLeuLysIleSerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrp 36
   |||
Db 1 TCTGAAATGTTCTGTAGGGTTCTGATACAGCTTACCAAGCTGATCGAGCTGG 60

QY 37 ValArgGlnMetProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSer 56
   |||
Db 61 GTGCCGCAATGCCCGGAAGGCTCGAGTGGATGGGATCATCATCTGTGACTGT 120

QY 57 AspThrLysTyrSerProSerPheGlnGlnValThrIleSerValAspLysSerVal 76
   |||
Db 121 GATACCAATACAGCCCTCTCCAAAGGCCAGTCCATCATCTCAGCCACAAGTCCATC 180

QY 77 SerThrAlaTyrLeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCys 96
   |||
Db 181 AGCACCGCTTACCTGACGTGAGACAGCTGAAGGCTCGGACACCGCATGTTACTGT 240

QY 97 AlaArgHisAspValGlyTyrCysSerSerSerAsnCyAlaLysTrpProGluTyrPhe 116
   |||
Db 241 GCGAGACGG-----GGTACTATGTTGGGGAGATTATTATTACTGG-----TTC 285

QY 117 GlnHisTrpGlyGlnGlyThrLeuValThrValSerSer 129
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Db 286 GACCCCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 324

RESULT 15
US-08-096-762-176
; Sequence 176, Application US/08096762
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-096-762-176

Alignment Scores:

Pred. No.:	2,92e-47	length:	383
Score:	465.50	Matches:	88
Percent Similarity:	85.0%	Conservative:	8
Best Local Similarity:	77.9%	Mismatches:	12
Query Match:	66.5%	Indels:	5
DB:	2	Gaps:	2

US-10-092-640-32 (1-129) x US-08-096-762-176 (1-383)

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DB	1	TCTCTGAAGATCTCCGTGAAGGTTCTGATACAGCTTACAGTACTGATCGGCTGG	60
QY	37	ValArgGlnMetProGlyLysGlyLysGlyLysMetGlyLeuIleTyrProGlyAspSer	56
DB	61	GTGCGCGAATGCGCGGAAAGCGCTGAGTGATGGAGGATCATCTATCTGCTGACTCT	120
QY	57	AspThrLysTyrSerProSerPheGlnGlyGlnValThrIleSerValAspLysSerVal	76
DB	121	GATACAGATACAGCCGCTCTTCCAAAGCCAGGTACATCTCAGCCGACAAAGTCCATC	180
QY	77	SerThrAlaTyrLeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCys	96
DB	181	ACACACCGCTACTGAGTGAAGACAGCTGAAGGCTCGACACCGCATGTATTAAGTGT	240
QY	97	AlaArgHisAspValGlyTyrCysSerSerSerAsnCysAlaLysTyrProGluTyrPhe	116
DB	241	GGAGAGCGG-----GGTACTATGTGGTGGGAGTTATTATTAAGTGG-----TTC	285
QY	117	GlnHisTyrGlyGlnGlyThrLeuValThrValSerSer	129
DB	286	GACCCCTGGGCGCAGGAACCCGTGTCACCGTCTCTCA	324

Search completed: May 25, 2006, 20:50:33
Job time: 169.7 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 20:50:52 ; Search time 1172.29 Seconds
(without alignments)
2028.220 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700

Sequence: 1 QVQLQSGMGLKPKGSLKI.....AKRPEYFGHWGQGLTVVSS 129

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-PPAN=human40.cdi -LIST=45 -LOCALIGN=200 -THR.SCORE=pct -THR.MAX=100
-THR.MIN=0 -ALIGN=15 -MODE=LOCALIGN -OUTFMT=pico -NORM=ext -HEADSIZE=500 -MINLEN=0
-USER=US10092640 @CCN 1.1 2326 @runat 25052006 155727 6087 -NCPU=6 -ICPU=3
-NO MAP -NEG SCORE=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YAPOP=10 -YAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.Main:*

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
1	700	100.0	765	3	US-09-888-721-35 Sequence 35, Appl

2	694	99.1	807	3	US-09-888-721-37	Sequence 37, Appl
3	694	99.1	846	3	US-09-888-721-39	Sequence 39, Appl
4	694	99.1	861	3	US-09-888-721-41	Sequence 41, Appl
5	694	99.1	873	3	US-09-888-721-45	Sequence 45, Appl
6	694	99.1	888	3	US-09-888-721-43	Sequence 43, Appl
7	539	77.0	369	13	US-11-009-731-102	Sequence 102, App
8	534.5	76.4	660	8	US-10-128-520-298	Sequence 298, App
9	532.5	76.1	666	8	US-10-128-520-293	Sequence 293, App
10	532.5	76.1	666	8	US-10-128-520-305	Sequence 305, App
11	532.5	76.1	672	8	US-10-128-520-308	Sequence 308, App
12	531	75.9	669	8	US-10-128-520-286	Sequence 286, App
13	530.5	75.8	379	8	US-10-041-860-69	Sequence 69, Appl
14	530.5	75.8	379	8	US-10-665-383-33	Sequence 33, Appl
15	529	75.6	669	8	US-10-128-520-307	Sequence 307, App
16	528.5	75.5	379	7	US-10-041-860-65	Sequence 65, Appl
17	528.5	75.5	379	7	US-10-041-860-77	Sequence 77, Appl
18	528.5	75.5	379	8	US-10-665-383-25	Sequence 25, Appl
19	528.5	75.5	379	8	US-10-665-383-49	Sequence 49, Appl
20	528.5	75.5	666	8	US-10-128-520-299	Sequence 299, App
21	526.5	75.2	666	8	US-10-128-520-294	Sequence 294, App
22	526.5	75.2	672	8	US-10-128-520-288	Sequence 288, App
23	526	75.1	369	7	US-10-173-551-3	Sequence 3, Appl
24	526	75.1	669	8	US-10-128-520-295	Sequence 295, App
25	525	75.0	669	8	US-10-128-520-302	Sequence 302, App
26	523.5	74.8	379	7	US-10-041-860-88	Sequence 88, Appl
27	523.5	74.8	379	8	US-10-665-383-69	Sequence 69, Appl
28	523.5	74.8	666	8	US-10-128-520-311	Sequence 311, App
29	520	74.3	462	16	US-11-009-840A-207	Sequence 207, App
30	520	74.3	462	16	US-11-009-873A-207	Sequence 207, App
31	520	74.3	462	16	US-11-009-873A-207	Sequence 207, App
32	519	74.1	351	16	US-11-157-494-35	Sequence 35, Appl
33	519	74.1	351	16	US-11-157-494-37	Sequence 37, Appl
34	519	74.1	469	8	US-10-395-894-26	Sequence 26, Appl
35	519	74.1	469	8	US-10-695-667-26	Sequence 26, Appl
36	519	74.1	469	10	US-10-976-352-26	Sequence 26, Appl
37	519	74.1	7558	8	US-10-395-894-5	Sequence 5, Appl
38	519	74.1	7558	8	US-10-695-667-5	Sequence 5, Appl
39	519	74.1	7558	10	US-10-976-352-5	Sequence 5, Appl
40	518.5	74.1	666	8	US-10-128-520-309	Sequence 309, App
41	518	74.0	388	7	US-10-041-860-71	Sequence 71, Appl
42	518	74.0	388	8	US-10-665-383-37	Sequence 37, Appl
43	518	74.0	669	8	US-10-128-520-291	Sequence 291, App
44	517	73.9	669	8	US-10-128-520-287	Sequence 287, App
45	512.5	73.2	354	7	US-10-181-324-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-888-721-35
; Sequence 35, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scheman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888, 721
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213, 653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide (C6.5
US-09-888-721-35

Alignment Scores:
Pred. No.: 3,33e-78      Length: 765
Score: 700.00           Matches: 129
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
DB: 3                  Gaps: 0

US-10-092-640-32 (1-129) x US-09-888-721-35 (1-765)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
DB 1 CAGGTGCACAGCTGTTCAGATACAGCTTACCACTGATCGCTGGGTGCGCCAGATC 60
QY 21 SerCySlyeGlySerGlyTyTyrSerPheThrSerTyTTPipIleAlaTrpValArgGlnMet 40
DB 61 TCCTGTAAAGGGTTCTGGATACAGCTTACCACTGATCGCTGGGTGCGCCAGATC 120
QY 41 ProGlyLysGlyLeuGlnTyTyrMetGlyLeuIleTyTyrProGlyAspSerAspThrLysTyTyr 60
DB 121 CCGGGAAAGGCGCTGAGATACATGGGGCTCATCTATCTGTGACTCTGACACCAATAC 180
QY 61 SerProSerPheGlnGlyValThrIleSerValAspLysSerValSerThrAlaTyTyr 80
DB 181 ACCCGGCTCTTCCAAAGGCCAGGTCAACATCTCAGTCGACAAAGTCCGTGACACTGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyTyrPheCysAlaArgHisAsp 100
DB 241 TTGCATATGAGCAGCTGTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB 301 GTGGGATATTGCAGATGATGTTCCAACTGCCGAAAGTGGCGTGAATACTTCCAGCATTTGGGGC 360

QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGCACCCCTGTGTACCGTCTCTCA 387

RESULT 2
US-09-888-721-37
; Sequence 37, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; TYPE: DNA
; LENGTH: 807
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide (C6ML3-9
; OTHER INFORMATION: sfv')
US-09-888-721-37
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Pred. No.: 2,06e-77      Length: 807
Score: 694.00           Matches: 127
Percent Similarity: 100.0%      Conservative: 2
Best Local Similarity: 98.4%      Mismatches: 0
Query Match: 99.1%      Indels: 0
DB: 3                  Gaps: 0

US-10-092-640-32 (1-129) x US-09-888-721-37 (1-807)

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DB 1 CAGGTGCACAGCTGTTCAGATACAGCTTACCACTGATCGCTGGGTGCGCCAGATC 60
QY 21 SerCySlyeGlySerGlyTyTyrSerPheThrSerTyTTPipIleAlaTrpValArgGlnMet 40
DB 61 TCCTGTAAAGGGTTCTGGATACAGCTTACCACTGATCGCTGGGTGCGCCAGATC 120
QY 41 ProGlyLysGlyLeuGlnTyTyrMetGlyLeuIleTyTyrProGlyAspSerAspThrLysTyTyr 60
DB 121 CCGGGAAAGGCGCTGAGATACATGGGGCTCATCTATCTGTGACTCTGACACCAATAC 180
QY 61 SerProSerPheGlnGlyValThrIleSerValAspLysSerValSerThrAlaTyTyr 80
DB 181 ACCCGGCTCTTCCAAAGGCCAGGTCAACATCTCAGTCGACAAAGTCCGTGACACTGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyTyrPheCysAlaArgHisAsp 100
DB 241 TTGCATATGAGCAGCTGTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB 301 GTGGGATATTGCAGATGATGTTCCAACTGCCGAAAGTGGCGTGAATACTTCCAGCATTTGGGGC 360

QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGCACCCCTGTGTACCGTCTCTCA 387

RESULT 3
US-09-888-721-39
; Sequence 39, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; TYPE: DNA
; LENGTH: 846
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6ML-3-9sfv'-LI-KDEL)
US-09-888-721-39

Alignment Scores:
Pred. No.: 2,19e-77      Length: 846
Score: 694.00           Matches: 127
Percent Similarity: 100.0%      Conservative: 2
Best Local Similarity: 98.4%      Mismatches: 0
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Query Match: 99.1% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-32 (1-129) x US-09-888-721-39 (1-846)

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DB 1 CAGGTGACGCTGCTGACGCTGCGGCGAGAGTAAAAAGCCGGGAGTCTTGAAATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTripleAlaTyrValArgGlnMet 40
DB 61 TCCTGTAAGGCTTCTGATACAGCTTACAGCTACAGATCGCTGGTGGCCGCAATG 120
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
DB 121 CCGGGAAAGCCCTGGAGTACATGGGGCTCATCTATCTGTGATCTTGACCAATAC 180
QY 61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 181 AGCCGCTCTTCCAAAGCCAGTCACTCATCTGACAGCAAGTCCGTGACACTGCTTAC 240
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 TTCGAATGAGAGCTGAGTGAAGCCCTCGACAGCGCGTGTATTTTGTGGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB 301 GTGGATATTGACGTAGTTCCTCAACTGGCAAGTGGCTGTAATACCTTCAGCATTTGGGCG 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGACCTGTGCTCACCGTCTCTCA 387
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RESULT 4

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US-09-888-721-41
; Sequence 41, Application US/09888721
; Patent No. US2002013290A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6ML3-9sfv'-L2-RDEL)
US-09-888-721-41
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Alignment Scores:

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Pred. No.: 2,24e-77 Length: 861
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 3 Gaps: 0
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US-10-092-640-32 (1-129) x US-09-888-721-41 (1-861)

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QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTripleAlaTyrValArgGlnMet 40
DB 61 TCCTGTAAGGCTTCTGATACAGCTTACAGCTACAGATCGCTGGTGGCCGCAATG 120
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
DB 121 CCGGGAAAGCCCTGGAGTACATGGGGCTCATCTATCTGTGATCTTGACCAATAC 180
QY 61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 181 AGCCGCTCTTCCAAAGCCAGTCACTCATCTGACAGCAAGTCCGTGACACTGCTTAC 240
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 TTCGAATGAGAGCTGAGTGAAGCCCTCGACAGCGCGTGTATTTTGTGGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB 301 GTGGATATTGACGTAGTTCCTCAACTGGCAAGTGGCTGTAATACCTTCAGCATTTGGGCG 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGACCTGTGCTCACCGTCTCTCA 387
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RESULT 5

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US-09-888-721-45
; Sequence 45, Application US/09888721
; Patent No. US2002013290A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6ML3-9sfv'-L2-nls)
US-09-888-721-45
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Alignment Scores:

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Pred. No.: 2,28e-77 Length: 873
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 3 Gaps: 0
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US-10-092-640-32 (1-129) x US-09-888-721-45 (1-873)

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DB 1 CAGGTGACGCTGCTGACGCTGCGGCGAGAGTAAAAAGCCGGGAGTCTTGAAATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTripleAlaTyrValArgGlnMet 40
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Db      121 TCTCTAAGAGGTTCTGGATACGCTTTACCACTGATGCTGCTGGGTGCGCCAGATG 120
Qy      41 ProGlyLysGlyLeuGluIuTyMetGlyLeuIleTyProGlyAspSerAspThrIleTy 60
Db      121 CCGGGGAAAGGCTCGGATACATGGGGCTCATCTATCTCGTGACTCTGACACCAATAC 180
Qy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrIleTy 80
Db      181 AGCCGCTCTTCCAAAGGCCAGGTCACATCTGACATGCAAGTCCGTCAGCACTGCTAC 240
Qy      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyPheCysAlaArgHisAsp 100
Db      241 TTGCATGAGAGCAGCTGTAAGCCCTCGACACGCCGCTGATTTTGTGCGAGACATGAC 300
Qy      101 ValGlyTyCySerSerSerAsnCysAlaTyStrpProGluTyPheGlnHisTrpGly 120
Db      301 GTGGGATATTGAGATGATTCCAATGCGCAAGTGGCTGAATATCTTCAGCATTTGGGCG 360
Qy      121 GlnGlyThrLeuValThrValSerSer 129
Db      361 CAGGGACCCCTGTGTCACCGTCTCTCA 387

RESULT 6
US-09-888-721-43
; Sequence 43, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scheman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
US-09-888-721-43

Alignment Scores:
Pred. No.: 2,33e-77 Length: 888
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
Gaps: 0

US-10-092-640-32 (1-129) x US-09-888-721-43 (1-888)
Qy      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
Db      1 CAGGTGACAGCTGTGAGTCTGGGGGCAAGGTGAAAAAGCCCGGAGACTCTGAAAGATC 60
Qy      21 SerCyLysGlySerGlyTySerPheThrSerTyTrpIleAlaTrpValArgGlnMet 40
Db      61 TCTGTGAAGGTTCTGATACAGCTTACAGCTACTGATCGCTGGGGTGGCCAGATG 120
Qy      41 ProGlyLysGlyLeuGluIuTyMetGlyLeuIleTyProGlyAspSerAspThrIleTy 60

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Db      121 CCGGGGAAAGGCTCGGATACATGGGGCTCATCTATCCGTGGTACTGACACCAATATC 180
Qy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrIleTy 80
Db      181 AGCCGCTCTTCCAAAGGCCAGGTCACATCTCAGTCGACAACTCCGTGACGACTGCTAC 240
Qy      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyPheCysAlaArgHisAsp 100
Db      241 TTGCATGAGAGCAGCTGTAAGCCCTCGACACGCCGCTGATTTTGTGCGAGACATGAC 300
Qy      101 ValGlyTyCySerSerSerAsnCysAlaTyStrpProGluTyPheGlnHisTrpGly 120
Db      301 GTGGGATATTGAGATGATTCCAATGCGCAAGTGGCTGAATATCTTCAGCATTTGGGCG 360
Qy      121 GlnGlyThrLeuValThrValSerSer 129
Db      361 CAGGGACCCCTGTGTCACCGTCTCTCA 387

RESULT 7
US-11-009-731-102
; Sequence 102, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shrikant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vandipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MX1-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-009-731-102

Alignment Scores:
Pred. No.: 3.3e-58 Length: 369
Score: 539.00 Matches: 101
Percent Similarity: 89.9% Conservative: 15
Best Local Similarity: 78.3% Mismatches: 7
Query Match: 77.0% Indels: 6
Gaps: 3

US-10-092-640-32 (1-129) x US-11-009-731-102 (1-369)
Qy      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
Db      1 GAGGTGACAGCTGTGAGTCTGGAGACAGAGTGAAGAAAAAGCCCGGAGACTCTGAAAGATC 60
Qy      21 SerCyLysGlySerGlyTySerPheThrSerTyTrpIleAlaTrpValArgGlnMet 40
Db      61 TCTGTGAAGGTTCTGATACACTTTCACACTGATGCTGCTGGGTGCGCCAGATG 120
Qy      41 ProGlyLysGlyLeuGluIuTyMetGlyLeuIleTyProGlyAspSerAspThrIleTy 60
Db      121 CCGGGGAAAGGCTCGGATGATGGGGGTCACTCTCCGCGTGAATATCTTCAGATGACATAC 180
Qy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrIleTy 80
Db      181 AGCCGCTCTTCCAAAGGCCAGGTCACATCTCAGTCGACAACTCCGTGACGACTGCTAC 240

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Oy      81 LeuGlnTrpSerSerLeuLysPProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db      241 CTCGAGTGGAGCGACCTGTAAGCCCTGGACACCGCATGTATTATCTGTGGAGA----- 299
Oy      101 ValGlyTyrCysSerSerSerSerAlaLysTrpProGluTyrPheGlnHisTrpGly 120
Db      295 ---GGATTATGTAGTGTGTACTG-----TACCA---TTCCTCCAGTACTGGGGC 342
Oy      121 GlnGlyThrLeuValThrValSerSer 129
Db      343 CAGGGCACCTGTGTCACCGTCTCTCC 369

RESULT 8
US-10-128-520-298
; Sequence 298, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 298
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-520-298

Alignment Scores:
Pred. No.:      2,63e-57      Length:      660
Score:          534.50      Matches:      99
Percent Similarity: 86.0%      Conservative: 12
Best Local Similarity: 76.7%      Mismatches: 7
Query Match:      76.4%      Indels:      11
DB:              8          Gaps:      1

US-10-092-640-32 (1-129) x US-10-128-520-298 (1-660)
Oy      1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 20
Db      1 CAGGTGCATTGGTTCAGAGCGCGCGGAAGTAAAAAACCAGGCGCAAAACCTGAAATTT 60
Oy      21 SerCysLysGlySerGlyTyrSerPheTrpSerTyrTrpIleAlaTrpValArgGlnMet 40
Db      61 AGCTCGAAAGGTTCGCGATATTCCTTTACGAGTATTTGGATTTGGCTGGGTGGCGCGCAGATG 120
Oy      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspTrpIleTyr 60
Db      121 CCTGGGAAGGTCCTCAGTGGAGTGAATTTATTCGGCGCATACGATACCCGTAT 180
Oy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db      181 TCTCCGAGCTTTCAGGGCCAGGTGACATTAGCGCGGATTAAGACATTACACCGCGTAT 240
Oy      81 LeuGlnTrpSerSerLeuLysPProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db      241 CTTCAATGAGACGCTTGAAAGCGACGAGTATGATGATTTATTCGGCGCGTTAA-- 297
Oy      101 ValGlyTyrCysSerSerSerSerAlaLysTrpProGluTyrPheGlnHisTrpGly 120
Db      298 -----CGTTATCCTCATATGTTGATTTTGGGGC 327

RESULT 9
US-10-128-520-293
; Sequence 293, Application US/10128520

```

```

; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-520-293

Alignment Scores:
Pred.No.:      4 77e-57      Length:      666
Score:         532.50       Matches:     100
Percent Similarity: 87.6%   Conservative: 13
Best Local Similarity: 77.5% Mismatches:    7
Query Match:    76.1%      Indels:        9
DB:             8          Gaps:           2

US-10-092-640-32 (1-129) x US-10-128-520-293 (1-666)

QY      1  GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1  CAGGTGCATTGGTTCACAGCGCCGCCGAAAGCAAAAACC GGCCGAACCTCGAATAAT 60

QY      21 SerCysLysGlySerGlyTyrSerPheThrSeryTrpIleAlaTrpValArgImet 40
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      61 AGCTCAAGAAGTTCCGAGATATCTTTACGACTATTGGATTGGCTGGGGCCAGATG 120

QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      121 CCTGGGAAGGCTCTGAGAGTAGGGCATTTATTTACCGGGCGCATGGCATTAACCGTTAT 180

QY      61 SerProSerPheGlnGlyGlnValThrlSerValAspLysSerValSerThrAlaTyr 80
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      181 TCTCCGAGCTTTCAGAGCCAGGTGCACATTAGCCGCGGATMAAACATTACACCGCTAT 240

QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      241 CTTCATGTGAGCAGCGCTTGAAACGAGCGCATGAGGCATGATATTGCCGGCGTTAT --- 297

QY      101 ValGlyTyrCysSerSerSerAsnCySalalysTrpProGlnTyrPheGlnHisTrpGly 120
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      298 -----TATGTATTACGATACT-----GCTTATTTGATTATTGGGGC 333

QY      121 GlnGlyThrLeuValThrValSerSer 129
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      334 CAAGGCACCTGTGTGACGGTTAGCTCA 360

RESULT 10
US-10-128-520-305
; Sequence 305, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Homo sapiens

```

US-10-128-520-305

Alignment Scores:
Pred. No.: 4.77e-57 Length: 666
Score: 532.50 Matches: 101
Percent Similarity: 84.8% Conservative: 11
Best Local Similarity: 76.5% Mismatches: 5
Query Match: 76.1% Indels: 15
DB: 8 Gaps: 2

US-10-092-640-32 (1-129) x US-10-128-520-305 (1-666)

```
OY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
DB 1 CAGGTGCATTGGTTTCAGAGCGCGCGGAGTCAAAAAACCGGCGAAAGCTGAAAAATT 60
OY 21 SerCyLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
DB 61 ACCTGCAAGGTTCCGAGTATTCCTTACGAGCTATTGGATTGGCTGGGTCGCCAGATG 120
OY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
DB 121 CCGGAAAGGCTCTCGAGATGCGATATTATTCGCGCGATGCGATACCCGTTAT 180
OY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 181 TCTCCAGCTTTCAGGCGCAGGTGACCATTAAGCGCGATTAAGACATTAACCGGTTAT 240
OY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 CTTCAATGAGCAGCCTGAAAGCGAGCATACGCGCATGATATTAATGCGCGCT----- 294
OY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 117
DB 295 -----CTTATCCGAGAGATCTTATTTATTTTGAAT 324
OY 118 HisTrpGlyGlnGlyTyrLeuValThrValSerSer 129
DB 325 TATTTGGGCGCAAGCGACCTGTGTGACGGTTAGCTCA 360
```

RESULT 11

US-10-128-520-308
; Sequence 308, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-520-308

Alignment Scores:

Pred. No.: 4.82e-57 Length: 672
Score: 532.50 Matches: 102
Percent Similarity: 86.8% Conservative: 10
Best Local Similarity: 79.1% Mismatches: 10
Query Match: 76.1% Indels: 7
DB: 8 Gaps: 2

US-10-092-640-32 (1-129) x US-10-128-520-308 (1-672)

```
OY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
DB 1 CAGGTGCATTGGTTTCAGAGCGCGCGGAGTCAAAAAACCGGCGAAAGCTGAAAAATT 60
```

```
OY 21 SerCyLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
DB 61 ACCTGCAAGGTTCCGAGTATTCCTTACGAGCTATTGGATTGGCTGGGTCGCCAGATG 120
OY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
DB 121 CCGGAAAGGCTCTCGAGATGCGATATTATTCGCGCGATGCGATACCCGTTAT 180
OY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 181 TCTCCAGCTTTCAGGCGCAGGTGACCATTAAGCGCGATTAAGACATTAAGCACCCGTTAT 240
OY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 CTTCAATGAGCAGCCTGAAAGCGAGCATACGCGCATGATATTAATGCGCGCTTTT--- 297
OY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB 298 GTTCTTATTAATGTTCT-----GTTCTTATTTTATTTATTTAGGGGC 339
OY 121 GlnGlyThrLeuValThrValSerSer 129
DB 340 CAAGGCACCTGTGTGACGGTTAGCTCA 366
```

RESULT 12

US-10-128-520-286
; Sequence 286, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-520-286

Alignment Scores:
Pred. No.: 7.43e-57 Length: 669
Score: 531.00 Matches: 101
Percent Similarity: 86.0% Conservative: 10
Best Local Similarity: 78.3% Mismatches: 10
Query Match: 75.9% Indels: 8
DB: 8 Gaps: 2

US-10-092-640-32 (1-129) x US-10-128-520-286 (1-669)

```
OY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
DB 1 CAGGTGCATTGGTTTCAGAGCGCGCGGAGTCAAAAAACCGGCGAAAGCTGAAAAATT 60
OY 21 SerCyLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
DB 61 ACCTGCAAGGTTCCGAGTATTCCTTACGAGCTATTGGATTGGCTGGGTCGCCAGATG 120
OY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
DB 121 CCGGAAAGGCTCTCGAGATGCGATATTATTCGCGCGATGCGATACCCGTTAT 180
OY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 181 TCTCCAGCTTTCAGGCGCAGGTGACCATTAAGCGCGATTAAGACATTAAGCACCGGTTAT 240
OY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
```



```
/ CURRENT FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: US 60/285,683
/ PRIOR FILING DATE: 2001-04-24
/ NUMBER OF SEQ ID NOS: 381
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 307
/ LENGTH: 669
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-128-520-307
```

Alignment Scores:

Pred. No.:	1,33e-56	Length:	669
Score:	529.00	Matches:	101
Percent Similarity:	84.1%	Conservative:	10
Best Local Similarity:	76.5%	Mismatches:	7
Query Match:	75.6%	Indels:	14
DB:	8	Gaps:	2

US-10-092-640-32 (1-129) x US-10-128-520-307 (1-669)

```
QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlyLeuLysLysProGlyGlnSerLeuLysIle 20
         |||||
         |::|
         1 CAGGTGCATTTGGTTCAGAGCGCGCGGAGTGAATAAAACCGGCGAAAGCCTGAATAATT 60
         |||||
         |::|
         21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
         |||||
         |::|
         DB      61 AGCTGCAAGAGTTCGCGATATTCCTTACGAGCTATTGATGGCTGGGTGGCGCCAGATG 120
         |||||
         |::|
         QY      41 ProGlyLysGlyLeuGlyTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
         |||||
         |::|
         DB      121 CCGGGAAGGCTCTCGAGTGAATGGCATTTATTATCCGGCGCATAGCATACCGCTTAT 180
         |||||
         |::|
         QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
         |||||
         |::|
         DB      181 TCTCCAGCTTCAGGGCCAGGTGACCATTAACCGCATTAAGCATTAAGCACCGCGTAT 240
         |||||
         |::|
         QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg----- 98
         |||||
         |::|
         DB      241 CTTCAATGAGAGCCTGTAAGCGAGCATACCGCATGATATTATGCGCGCTCTTCGT 300
         |||||
         |::|
         QY      99 --HisAspValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyrPheGln 117
         |||||
         |::|
         DB      301 GTTCATGAT-----TATGCTATGATTTTGAT 327
         |||||
         |::|
         QY      118 HistTrpGlyGlnGlyThrLeuValThrValSerSer 129
         |||||
         |::|
         DB      328 CTTGGGGCCAAAGGCACCTGATGACGTTAGCTCA 363
         |||||
         |::|
```

Search completed: May 25, 2006, 21:27:51
Job time : 1174.29 secs

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_pzn model

Run on: May 25, 2006, 20:51:32 ; Search time 20.425 Seconds
(without alignments)
1069.431 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700
Sequence: 1 QVQLQSGAELKKPGESLKI.....AKRPEYFQHWGQTLTVVSS 129

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA New -OPMT=fastcap -SUPEX=trnphn -MINMATCH=0.1
-LOOPT=0 -LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs802h
-USER=US10092640 @CGN 1.1.26 @runat_25052006.155730.6141 -NCPU=6 -ICPU=3
-NO MAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=100
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

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2: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US06_NEW_PUB.seq.*
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4: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US11_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	487	69.6	369	6 US-10-499-266-11	Sequence 11, Appl
2	406.5	58.1	378	7 US-11-211-917-41	Sequence 41, Appl
3	406.5	58.1	1416	7 US-11-211-917-45	Sequence 45, Appl
4	398.5	56.9	2094	7 US-11-155-444-1	Sequence 1, Appl1
5	398.5	56.9	2196	7 US-11-155-444-5	Sequence 5, Appl1
6	390.5	53.8	885	7 US-11-154-103-33	Sequence 33, Appl
7	374	53.4	420	7 US-11-183-218-61	Sequence 61, Appl
8	374	53.4	9209	7 US-11-183-218-58	Sequence 58, Appl
9	368.5	52.6	726	7 US-11-183-325-17	Sequence 17, Appl

10	368.5	52.6	756	7 US-11-330-353-17	Sequence 17, Appl
11	365.5	52.2	372	7 US-11-271-008-10	Sequence 10, Appl
12	364.5	52.1	333	7 US-11-216-033-13	Sequence 13, Appl
13	361.5	51.6	360	7 US-11-221-902-83	Sequence 83, Appl
14	358.5	51.2	354	7 US-11-297-317-12	Sequence 12, Appl
15	358.5	51.2	8687	7 US-11-297-317-15	Sequence 15, Appl
16	356.5	50.9	360	7 US-11-221-902-20	Sequence 20, Appl
17	355.5	50.8	354	7 US-11-297-317-11	Sequence 11, Appl
18	355.5	50.8	8687	7 US-11-297-317-16	Sequence 16, Appl
19	352	50.3	807	7 US-11-219-563-23	Sequence 23, Appl
20	352	50.3	1578	7 US-11-219-563-131	Sequence 131, Appl
21	352	50.3	1701	7 US-11-106-662-10	Sequence 10, Appl
22	352	50.3	360	7 US-11-221-902-82	Sequence 82, Appl
23	349.5	49.9	360	7 US-11-216-033-9	Sequence 9, Appl1
24	341.5	48.8	334	7 US-11-297-317-6	Sequence 6, Appl1
25	338.5	48.4	354	7 US-10-981-300-15	Sequence 15, Appl
26	338.5	48.4	1362	6 US-11-183-325-19	Sequence 19, Appl
27	335.5	47.9	726	7 US-11-183-325-13	Sequence 13, Appl
28	335	47.9	408	7 US-11-315-067-1	Sequence 1, Appl1
29	335	47.9	408	7 US-11-315-067-7	Sequence 7, Appl1
30	333	47.6	873	7 US-11-154-103-35	Sequence 35, Appl
31	331.5	47.4	1628	7 US-11-293-697-1846	Sequence 1846, Ap
32	331	47.3	1602	7 US-11-293-697-1849	Sequence 1849, Ap
33	330.5	47.2	360	7 US-11-254-679-16	Sequence 16, Appl
34	329	47.0	1613	7 US-11-293-697-1839	Sequence 1839, Ap
35	326	46.6	873	7 US-11-154-103-36	Sequence 36, Appl
36	326	46.6	1618	7 US-11-293-697-1845	Sequence 1845, Ap
37	325	46.4	1613	7 US-11-293-697-1848	Sequence 1848, Ap
38	323.5	46.2	366	7 US-11-254-679-73	Sequence 73, Appl
39	322.5	46.1	378	7 US-11-254-679-49	Sequence 49, Appl
40	322	46.0	1598	7 US-11-293-697-1642	Sequence 1642, Ap
41	321	45.9	369	7 US-11-254-679-12	Sequence 12, Appl
42	319.5	45.6	873	7 US-11-254-679-69	Sequence 69, Appl
43	319.5	45.6	873	7 US-11-154-103-32	Sequence 32, Appl
44	318.5	45.5	354	7 US-11-219-563-73	Sequence 73, Appl
45	318.5	45.5	354	7 US-11-219-563-75	Sequence 75, Appl

ALIGNMENTS

US-10-499-266-11
; Sequence 11, Application US/10499266
; Publication No. US20060088531A1
; GENERAL INFORMATION:
; APPLICANT: Smethurst, Peter Alexander
; APPLICANT: Overhand, Willem Hendrik
; APPLICANT: Fardale, Richard William
; TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST HUMAN
; FILE REFERENCE: 191134.401USPC
; CURRENT APPLICATION NUMBER: US/10/499,266
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/GB02/05755
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: GB 0130543.2
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-499-266-11

Alignment Scores:
Pred. No.: 1,1e-48
Score: 487.00
Percent Similarity: 78.9%
Best Local Similarity: 79.7%
Query Match: 69.6%
DB: 6
Length: 369
Matches: 94
Conservative: 11
Mismatch: 14
Indels: 14
Gaps: 2

```

US-10-092-640-32 (1-129) x US-10-499-266-11 (1-369)
QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
DB      1 CAGGTACACACTGTCAGACGTCAGGGGCGAGGTGAAGAAAGCCGGGGAGTCTCTGAAGATC 60
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
DB      61 TCTGTACAGGCTTCTGGATACAGCTTTCAGTACTGATGCGCTGGGGTGGCCAGATG 120
QY      41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
DB      121 CCGGGGAAAGGCGCTGGAGTTGATGGGATCATCTATCCGTGAGCTCTGATGCAAGATC 180
QY      61 SerProserPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB      181 ACCCGGCTCTTCCAGGCGCAGGTCACCTTCTCGCCGACAGCCATTAACACCGCTAT 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB      241 TTGCGATGGAGACCTTGAAAGGCTTGACACCGCATATATATGTGCGAGACA--- 297
QY      101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyr-----Phe 116
DB      298 -----GGGAAACCTGGAGCTACTATTGGTGTCTTT 330
QY      117 GlnHisTrpGlyGlnGlyThrLeuValThrValSerSer 129
DB      331 GATGTCTGGGGCCAGGACAAATGTCACCGTCTCTTCA 369

RESULT 2
US-11-211-917-41
; Sequence 41, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-41

Alignment Scores:
Pred. No.:      2,82e-39      Length:      378
Score:          406.50      Matches:      75
Percent Similarity: 76.9%      Conservative: 25
Best Local Similarity: 57.7%      Mismatches:  25
Query Match:    58.1%      Indels:      5
DB:             7          Gaps:      2

US-10-092-640-32 (1-129) x US-11-211-917-41 (1-378)
QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
DB      1 CAGGTACACACTGTCAGTCTGGGCTGAGTGAAGAAGCTTGGGGCTCTCAGTGAAGATC 60
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
DB      61 TCTGTCAAGGCTTCTGGATACACCTTACCGGCTACTATATATGCACTGGGTGCGACAGGCC 120

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QY      41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
DB      121 CTTGACAAAGGCTTGAATGATGGATGGATGCAACCTTGACAGTGGTGGCAAACTAT 180
QY      61 SerProserPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB      181 GCACAGAAAGTTTCAAGGCGAGGTCACCATGACACAGGACACCTCATCAGCACACCTAC 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg--His 99
DB      241 ATGAGACTGAACAGGCTGAGATCTGACGACAGCGCGGTGTAATTACTGTGCGAGAGATGAG 300
QY      100 AspValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyrPheGlnHisTrp 119
DB      301 CCCCTGAGATATTTGATCTTAATGTGTATGCTCC-----TACTTGTACTACTGG 348
QY      120 GlyGlnGlyThrLeuValThrValSerSer 129
DB      349 GGCAGGAGACCTTGTCACCGTCTCTCTCA 378

RESULT 3
US-11-211-917-45
; Sequence 45, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-45

Alignment Scores:
Pred. No.:      1.72e-38      Length:      1416
Score:          406.50      Matches:      75
Percent Similarity: 76.9%      Conservative: 25
Best Local Similarity: 57.7%      Mismatches:  25
Query Match:    58.1%      Indels:      5
DB:             7          Gaps:      2

US-10-092-640-32 (1-129) x US-11-211-917-45 (1-1416)
QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
DB      58 CAGGTACAGGCTTGTGATGATGGATGGATGCAACCTTGACAGTGGTGGCAAACTAT 117
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
DB      118 TCTGTCAAGGCTTCTGGATACACCTTACCGGCTACTATATGCACTGGGTGCGACAGGCC 177
QY      41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
DB      178 CTTGACAAAGGCTTGAATGATGGATGGATGCAACCTTGACAGTGGTGGCAAACTAT 237
QY      61 SerProserPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB      238 GCACAGAAAGTTTCAAGGCGAGGTCACATGACAGGACACGTCATGACGACAGCTTAC 297

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QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValThrPheCysAlaArg---His 99
Db      298 ATGGAGCTGAACGAGCTGAGATCTGACGACGCGGTGATTACTGTGGAGAGATCAG 357
QY      100 AspValGlyTyrCysSerSerAsnCyAlaLysTrpProGluTyrPheGlnHisTrp 119
Db      358 CCCCTAGGATATTGTACTATATGATGATGCTCC-----TACTTTGACTACTG 405
QY      120 GlyGlnGlyThrLeuValThrValSerSer 129
Db      406 GGCAGGAGAACCTGTGTCACCGTCTCTCA 435

RESULT 4
US-11-155-444-1
/ Sequence 1, Application US/11155444
/ Publication No. US20060104971A1
/ GENERAL INFORMATION:
/ APPLICANT: GARBER, ELLEN
/ APPLICANT: BAILLY, VERONIQUE
/ APPLICANT: BROWNING, JEFFREY L.
/ TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
/ FILE REFERENCE: BGN168CN
/ CURRENT APPLICATION NUMBER: US/11/155,444
/ PRIOR FILING DATE: 2005-06-17
/ PRIOR APPLICATION NUMBER: PCT/US03/041393
/ PRIOR FILING DATE: 2003-12-22
/ PRIOR APPLICATION NUMBER: 60/435,154
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 60/435,185
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 1
/ LENGTH: 2094
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of
/ OTHER INFORMATION: hucBE11/huBHA10 bispecific-1 antibody construct
US-11-155-444-1

Alignment Scores:
Pred. No.: 2,52e-37 Length: 2094
Score: 398.50 Matches: 75
Percent Similarity: 75.2% Conservative: 22
Best Local Similarity: 58.1% Mismatches: 19
Query Match: 56.9% Indels: 13
Db: 7 Gaps: 2

US-10-092-640-32 (1-129) x US-11-155-444-1 (1-2094)
QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
Db      1378 CAGGTCACACTGCTGAGTCTGAGCTGAGTGAAGAAGCTGGTCTCAGAGAAAGTG 1437
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db      1438 TCCTGCAAGGCTTCTGCTGACCTTTCACAACTACTATTGCACTGGGTGAGGCGAGCC 1497
QY      41 ProGlyLysGlyLeuGlnLysTrpMetGlyLeuIleTyrProGlyLysSerSerAspThrLysIle 60
Db      1498 CCTGGACAGGGAATTAGTGAGATGGATGATTATCTCGGAATGTTTCATGCTCAGTAC 1557
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db      1558 AATGAGAACTTCAAGGCGAGGCTCAATCATCTGACGACAAATCCACGACAGAGCTTAC 1617
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db      1618 ATGGAGCTCAGAGCTGAGCTGAGATTAATGCGGCTGATTAATGCTCAAGA----- 1671
QY      101 ValGlyTyrCysSerSerSerSerAsnCyAlaLysTrpProGluTyrPheGlnHisTrpGly 120
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Db      1672 -----TCTGTG---GAAGCTTTCTCTTACTGAGGC 1698
QY      121 GlnGlyThrLeuValThrValSerSer 129
Db      1699 CAAGGAGCACGCTCACCGCTCTCTCA 1725

RESULT 5
US-11-155-444-5
/ Sequence 5, Application US/11155444
/ Publication No. US20060104971A1
/ GENERAL INFORMATION:
/ APPLICANT: GARBER, ELLEN
/ APPLICANT: BAILLY, VERONIQUE
/ APPLICANT: BROWNING, JEFFREY L.
/ TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
/ FILE REFERENCE: BGN168CN
/ CURRENT APPLICATION NUMBER: US/11/155,444
/ PRIOR FILING DATE: 2005-06-17
/ PRIOR APPLICATION NUMBER: PCT/US03/041393
/ PRIOR FILING DATE: 2003-12-22
/ PRIOR APPLICATION NUMBER: 60/435,154
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 60/435,185
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 5
/ LENGTH: 2196
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: hucBE11/huBHA10
/ OTHER INFORMATION: bispecific-2 antibody construct
US-11-155-444-5

Alignment Scores:
Pred. No.: 2,69e-37 Length: 2196
Score: 398.50 Matches: 75
Percent Similarity: 75.2% Conservative: 22
Best Local Similarity: 58.1% Mismatches: 19
Query Match: 56.9% Indels: 13
Db: 7 Gaps: 2

US-10-092-640-32 (1-129) x US-11-155-444-5 (1-2196)
QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
Db      1480 CAGGTCACACTGCTGAGTCTGAGCTGAGTGAAGAAGCTGGTCTCAGAGTGAAGTG 1539
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db      1540 TCCTGCAAGGCTTCTGCTGACCTTTCACAACTACTATTGCACTGGGTGAGGCGAGCC 1599
QY      41 ProGlyLysGlyLeuGlnLysTrpMetGlyLeuIleTyrProGlyLysSerSerAspThrLysIle 60
Db      1600 CCTGGACAGGGAATTAGTGAGATGGATGATTATCTCGGAATGTTTCATGCTCAGTAC 1659
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db      1660 AATGAGAACTTCAAGGCGAGGCTCAATCATCTGACGACAAATCCACGACAGAGCTTAC 1719
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db      1720 ATGGAGCTCAGAGCTGAGCTGAGATTAATGCGGCTGATTAATGCTCAAGA----- 1773
QY      101 ValGlyTyrCysSerSerSerSerAsnCyAlaLysTrpProGluTyrPheGlnHisTrpGly 120
Db      1774 -----TCTGTG---GAAGCTTTCTCTTACTGAGGC 1800
QY      121 GlnGlyThrLeuValThrValSerSer 129
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Db      1801 CAAGGAGCAGCGTCACTCTCTCA 1827

RESULT 6
US-11-154-103-33
; Sequence 33, Application US/11154103
; Publication No. US20060099205A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-11-154-103-33

Alignment Scores:
Pred. No.:      6,66e-37      Length:      885
Score:          390.50      Matches:      77
Percent Similarity: 75.6%      Conservative: 22
Best Local Similarity: 58.8%      Mismatches: 25
Query Match:    55.8%      Indels:      7
DB:              7          Gaps:          2

US-10-092-640-32 (1-129) x US-11-154-103-33 (1-885)

QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
      ::::::::::::::::::::
Db      67 GAGGTGCACTGCTGTCAGTCTGGGGCTGAGTGAAAGCCTGGTCTCGTGAAGGTC 126
      ::::::::::::::::::::
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
      ::::::::::::::::::::
Db      127 TCCTGCAAGGCTTCTTGAGGACCTTCACGACGATGCTATGCTGAGTGGGAGCAGGCC 186
      ::::::::::::::::::::
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
      ::::::::::::::::::::
Db      187 CCTGGACAAAGGCTTGAAGTGGATGGAGGAGATCATCTCTTGGTACAGCAACTAC 246
      ::::::::::::::::::::
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
      ::::::::::::::::::::
Db      247 GCACAGAAAGTCCAGGCGACAGTCAAGATTACCGCGAATCCACGAGCAGGCTTAC 306
      ::::::::::::::::::::
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
      ::::::::::::::::::::
Db      307 ATGAGAGTGAAGCCTGAGATCTGAGACACGCGCTGTATATTAATGTCGAGAGAGG 366
      ::::::::::::::::::::
QY      101 ValGlyTyrCysSerSerSerSerAsnCysAlaLysTrpProGlyLysTyr-----PheGlnHis 118
      ::::::::::::::::::::
Db      367 GGGGCCATATTGTAAGTACACAGCTGC-----TATGGGCTTTTGATATC 411
      ::::::::::::::::::::
QY      119 TrpGlyGlnGlyThrLeuValThrValSerSer 129
      ::::::::::::::::::::
Db      412 TGGGGCCAAGGCACTCGTGTACACCGTCTCTCA 444
      ::::::::::::::::::::

RESULT 7
US-11-183-218-61
; Sequence 61, Application US/11183218
; Publication No. US2006008906A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-183-218-61

Alignment Scores:
Pred. No.:      2.03e-35      Length:      420
Score:          374.00      Matches:      74
Percent Similarity: 71.3%      Conservative: 18
Best Local Similarity: 57.4%      Mismatches: 29
Query Match:    53.4%      Indels:      8
DB:              7          Gaps:          2

US-10-092-640-32 (1-129) x US-11-183-218-61 (1-420)

QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
      ::::::::::::::::::::
Db      58 CAGGTAAACATGACACACCTGGGGCTGAGTGAAGCCTGGGCTCACTGAAGATG 117
      ::::::::::::::::::::
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
      ::::::::::::::::::::
Db      118 TCCTGCAAGGCTTCTTGAGGACCTTCACGACGATGCTATGCTGAGTGGGAGATGATCTTCTAC 177
      ::::::::::::::::::::
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
      ::::::::::::::::::::
Db      178 CCTGGTCGGGGCTGGAATGATGAGTGAAGTATTTATCCGGAATGATGATCTTCTAC 237
      ::::::::::::::::::::
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
      ::::::::::::::::::::
Db      238 AATCAAGATTCAAAGGACACACATTCAGTCAAGCAATCTCCAGACACAGCTTAC 297
      ::::::::::::::::::::
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
      ::::::::::::::::::::
Db      298 ATGACAGTCAAGGCTTCACTGATCTGAGATCTGCGCTTATCTATCTGCAAGA----- 351
      ::::::::::::::::::::
QY      101 ValGlyTyrCysSerSerSerSerAsnCysAlaLysTrpProGlyLysTyrPheGlnHisTrpGly 120
      ::::::::::::::::::::

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Db      358 -----TCGACTACTACGGCGGTAAGTCTG-----TACTTCAATGCTCGGGC 399
Qy      121 GlnGlyThrLeuValThrValSerSer 129
          ||||| ||||| ||||| |||||
Db      394 GCAGGACCCACGGCTACCGTCTCTGCA 420

RESULT 8
US-11-183-218-58
; Sequence 58, Application US/11183218
; Publication No. US20060088906A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 9209
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-183-218-58

Alignment Scores:
Pred. No.: 1,386-33 Length: 9209
Score: 374.00 Matches: 74
Percent Similarity: 71.3% Conservative: 18
Best Local Similarity: 57.4% Mismatches: 29
Query Match: 53.4% Indels: 8
DB: 7 Gaps: 2

US-10-092-640-32 (1-129) x US-11-183-218-58 (1-9209)
Qy      1 GlnValGlnLeuLglnSerGlyValGlnLeuLysProGlyGlnSerLeuLysIle 20
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2458 CAGGTACAACTCTCAGACAGCGCTGGGCTAGCTGTGGAAGCCCTGGGGCCCTCAGTGAAGATG 2511
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnIle 40
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2518 TCCTCCAAAGGCTTCTGGCTACACATTTCACAGTTACATATGCACCTGGGTAAACAGACA 2577
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      41 ProGlyLysGlyLeuGlnLysTrpMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2578 CTGTGTGGGGGCTGTGAATGAGATTGAGCTATTATCCCGGAATAGTGATATCTTCTTC 2637
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Oy	61serProsePheGlnGIgInValThrIleSerValAspLysSerValSerThralatYr	80
Dd	2638 AATCAGAAGCTTCAAAAGGACCGCCACATTGACTGCAGACAATTCCTCCAGCACAGCCTAC	2697
Oy	81 LeuGlnTrpSerSerLeuLysProSerAaspSeralalaValTyrPheCysAlaargHisasp	100
Dd	2698 ATGACAGCTCAGAGCCTGACATCTGAGGACCTGGCGGTCTATACTGTGCCAAGA-----	2751
Oy	101 ValGIgTyrCysSerSerSerasnCysAlaalystrPrGlnIutryrhGlnHistrPGly	120
Dd	2752 -----TCGACTTACTACGGCGGTGACTCG-----TACTTCAATGTCGTGGGC	2793
Oy	121 GlnGIgTyrLeuValThrValSerSer	129
Dd	2794 GCAGGACCACCGGTACCCGTCTCTGCA	2820
 RESULT 9 US-11-183-325-17 ; Sequence 17, Application US/11183325 ; Publication No. US20060104898A1 ; GENERAL INFORMATION: ; APPLICANT: Vanderbilt University ; APPLICANT: Hallahan, Dennis E ; APPLICANT: Qu, Shmian ; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES ; FILE REFERENCE: 1242/47/2/2 CIP ; CURRENT APPLICATION NUMBER: US/11/183, 325 ; PRIOR FILING DATE: 2005-07-15 ; PRIOR APPLICATION NUMBER: US 60/328123 ; PRIOR FILING DATE: 2001-10-03 ; PRIOR APPLICATION NUMBER: US 10/259, 087 ; PRIOR FILING DATE: 2002-09-27 ; NUMBER OF SEQ ID NOS: 56 ; SOFTWARE: PatentIn version 3.3 ; SEQ ID NO 17 ; LENGTH: 726 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Artificial antibody ligand number 1 ; NAME/KEY: CDS ; LOCATION: (1) .. (726) US-11-183-325-17		
 Alignment Scores:		
Pred. No.:	1.88e-34	Length: 726
Score:	368..50	Matches: 73
Percent Similarity:	71.3%	Conservative: 19
Best Local Similarity:	56.6%	Mismatches: 26
Query Match:	52.6%	Indels: 11
DB:	7	Gaps: 2
 US-10-092-640-32 (1-129) x US-11-183-325-17 (1-726)		
Oy	1 GlnValGlnLeuLeuGlnSerGIgValaGlnLeuLysLysProGIgLysSerLeuLysile	20
Dd	7 CAGGTGAACCTGCACGACGACTGGGGCTTAGCTTGAGATGCTGGGGCTTCACGTGAAGATG	66
Oy	21 SerCysLysGIgLSerGIgTyrSerPheThrSerTyrTPripilaalatrPVaIargGlnmet	40
Dd	67 TCCTGCAGAGGCTTCTGGCTTACACATTTCACTGACTGACTGATGATGCACTGGGTTGAAGCAGAGG	126
Oy	41 ProGIgLYsgLYLeuGlnIutryrMeGilyLeuileTyrProGIgaSpSerAaspPhyrlatYr	60
Dd	127 CCTGGACACAGGCTTGTAGTGTATGGAGCGATTAATCTTGATGTATATCTGACTAC	186
Oy	61 serProserPheGlnGIgInValThrIleSerValAspLysSerValSerThralatYr	80
Dd	187 AATCAAAGTTCAAGGCGCAGGACCATTTGACTGTAGACGATCTCCAGCACAGCCTAC	246
Oy	81 LeuGlnTrpSerSerLeuLysProSerAaspSeralalaValTyrPheCysAlaargHisasp	100

```

Db      247 ATGCAGCTAGACAGCTGACATCTGAGAGCTCGCGCTATTACTGTGCAAGAGA--- 303
Qy      101 VALGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
Db      304 ---GGCTACTATAGCGCA-----TTGATTACTGTGGGC 333

```

```

Qy      121 GlnGlyThrLeuValThrValSerSer 129
Db      334 CAAGGAGTACGCTCACGCTCTCTCA 360

```

RESULT 10

```

US-11-330-353-17
; Sequence 17, Application US/11330353
; Publication No. US20060105429A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice

```

```

; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES

```

```

; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcoia Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/330,353
; FILING DATE: 12-Jan-2006
; CLASSIFICATION: <Unknown>

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,624
; FILING DATE: 10-Sep-2002
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-Jan-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-Jul-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-Jan-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-Jan-1993

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph. D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST93006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808

```

```

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

```

```

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..752
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-11-330-353-17

```

Alignment Scores:

```

Pred. No.: 1,986-34 Length: 756
Score: 368.50 Matches: 73
Percent Similarity: 60.7% Conservative: 19
Best Local Similarity: 54.5% Mismatches: 27
Query Match: 52.6% Indels: 15
DB: 7 Gaps: 2

```

US-10-092-640-32 (1-129) x US-11-330-353-17 (1-756)

```

Qy      1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuValSerProGlyGlnSerLeuValSile 20
Db      12 CAGGTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCT 71
Qy      21 SerCysLeuSerGlySerGlyTyrSerSerSerSerSerSerSerSerSerSerSerSer 40
Db      72 TCTCTCAAGCTTCTGGCTGACGATTCAGTACGCTTGTGATTAACCTGATTAACCTGATTAAC 131
Qy      41 ProGlyLysGlyLeuGlnLysMetGlyLeuLysLeuLysTyrProGlyLysSerSerSerSer 60
Db      132 CCTGACAGAGGCTTGTGATGATTTATTCCTGAGATGAGATGAGATGAGATGAGATGAGAT 191
Qy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db      192 AATGGGAAGTTCAGAGGCAAGGCACTGACGCGGACAGATCCAGCAGCAGCTTAC 251
Qy      81 LeuGlnTyrSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 99
Db      252 ATGCAGCTCAGCAGCTGACCTCTGTGGCTTGTGGCTTGTGGCTTGTGGCTTGTGGCTTGT 311
Qy      100 -----AspValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSer 115
Db      312 AATAGTTCAGACGAGAGGGTTACTATGCT----- 341
Qy      116 PheGlnHisTyrPheGlnGlyThrLeuValThrValSerSer 129
Db      342 ATGACCTACTGGGGCAAGGACCAAGCTGACCGCTCTCTCA 383

```

RESULT 11

```

US-11-271-008-10
; Sequence 10, Application US/11271008
; Publication No. US20060093610A1
; GENERAL INFORMATION:
; APPLICANT: Lang, Alois B.
; APPLICANT: Horn, Michael P.
; APPLICANT: Imboden, Martin A.

```

```

; TITLE OF INVENTION: Human Monoclonal Antibody Specific for Lipopolysaccharides (LPS)
; FILE REFERENCE: 29474-5015
; CURRENT APPLICATION NUMBER: US/11/271,008
; FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: PCT/EP2004/004485
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: EP 03 010 836.9
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 10
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-271-008-10

```

Alignment Scores:

```

Pred. No.: 1,696-34 Length: 372
Score: 365.50 Matches: 71
Percent Similarity: 69.8% Conservative: 19
Best Local Similarity: 55.0% Mismatches: 34
Query Match: 52.2% Indels: 5
DB: 7 Gaps: 2

```

US-10-092-640-32 (1-129) x US-11-271-008-10 (1-372)

Qy 1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuValSerProGlyGlnSerLeuValSile 20

```

Db      1 CAGGCCAGCTGCTGCAAGTCTGGGGCTGAAGTGAAGAGCTGGAGCTCAAGTGAAGCTC 60
Qy      21 SerCyAluSgIySerGlyTyTrSerPheThrSerTyTrPleAlaTrpValArgGlnMet 40
Db      61 TCCTGTAAGGCTTCTGGATACACCTTCATCGGCTATTGATGACACTGGGTGGCAGAGGCC 120
Qy      41 ProGlyLysGlyLeuGluTyTrMetGlyLeuIleTyTrProGlyAspSerAspThrLysTyTr 60
Db      121 CCTGGACAAAGGCTGAGTGAATGGACGATCAACCTTAACAGTGTGGCAAAAGTAT 180
Qy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyTr 80
Db      181 GTACAGAACTTCAAGGCGAGGCTACCGTACCAAGGACACGTCCTCATCAGACAGCTTAC 240
Qy      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyTrPheCysAlaArgHisAsp 100
Db      241 ATGAGACTGCAACTGCGTACATCTGACACACGCGCTTATTACTGTGGAGAGGAGG 300
Qy      101 ValGlyTyTrCysSerSerSerSerSerValAlaLysTrpProGluTyTrPheGlnHisTrpGly 120
Db      301 CTTGGT-----TGCGTGTGTGATTGCTAT-----GAGGTCTTAGATTACTGGGGC 345
Qy      121 GlnGlyThrLeuValThrValSerSer 129
Db      346 CAGGGAACCTGCTGCTCACCCTCTCTCA 372

RESULT 12
US-11-216-033-13
; Sequence 13, Application US/11216033
; Publication No. US20060104899A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS J.
; APPLICANT: GRIFFITHS, GARY L.
; APPLICANT: MCBRIDE, WILLIAM J.
; APPLICANT: LEUNG, SHUI-ON
; APPLICANT: OU, ZHENGXING
; TITLE OF INVENTION: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR
; TITLE OF INVENTION: USE WITH BI-SPECIFIC ANTIBODIES
; FILE REFERENCE: 40923-0074US4
; CURRENT APPLICATION NUMBER: US/11/216,033
; PRIOR FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US/09/823,746
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/337,756
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 13
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(333)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic humanized
; OTHER INFORMATION: Mu-9 heavy chain variable region nucleotide sequence
US-11-216-033-13

Alignment Scores:
Pred. No.: 1,89e-34 Length: 333
Score: 364.50 Matches: 69
Percent Similarity: 68.8% Conservative: 19
Best Local Similarity: 53.9% Mismatches: 23
Query Match: 52.1% Indels: 17
Db: 7 Gaps: 1

US-10-092-640-32 (1-129) x US-11-216-033-13 (1-333)
Qy      2 ValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIleSer 21
Db      1 GTGCAAGCTCAGCAGATCAGAGCTGAGTGAAAGAAAGCTGGAGCTCATGAAAGCTCTCC 60

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Qy      22 CyAluSgIySerGlyTyTrSerPheThrSerTyTrPleAlaTrpValArgGlnMetPro 41
Db      61 TGCAGAGCTTCTGATACACCTTCACCTGAGTATGTTATTACTGGGTAAAGAGAGACT 120
Qy      42 GlyLysGlyLeuGluTyTrMetGlyLeuIleTyTrProGlyAspSerAspThrLysTyTrSer 61
Db      121 GGAAGAGCTTAAAGAGTATGAGAGATTATTCCTGGAAGTGGTAGTACTTCTCAAT 180
Qy      62 ProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyTrLeu 81
Db      181 GAAATTTCAAGGCGAAGGCGCAATCATCTCGTACAAATCCACTAACAAGCTTACATG 240
Qy      82 GlnTrpSerSerLeuLysProSerAspSerAlaValTyTrPheCysAlaArgHisAspVal 101
Db      241 GAGCTCAGCAGCTTGAATCTGAGACACACTGCGCTTCTATTCTGTCAAGAGAGAGATCTT 300
Qy      102 GlyTyTrCysSerSerSerSerSerSerValAlaLysTrpProGluTyTrPheGlnHisTrpGly 121
Db      301 GGG-----GGCCAA 309
Qy      122 GlyThrLeuValThrValSerSer 129
Db      310 GGGTCTGTGTCACCGTCTCTTCA 333

RESULT 13
US-11-221-902-83
; Sequence 83, Application US/11221902
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGA
; FILE REFERENCE: 04000-031285
; CURRENT APPLICATION NUMBER: US/11/221,902
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 83
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(360)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequences
; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
US-11-221-902-83

Alignment Scores:
Pred. No.: 4,72e-34 Length: 360
Score: 361.50 Matches: 72
Percent Similarity: 72.1% Conservative: 21
Best Local Similarity: 55.8% Mismatches: 27
Query Match: 51.6% Indels: 9
Db: 7 Gaps: 2

US-10-092-640-32 (1-129) x US-11-221-902-83 (1-360)
Qy      1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 20
Db      1 CAGTCCAGAGCTGCTGCAAGTCTGAGCCCAAGGAAAGAAAGCTGGGGCTTCAAGTGAAGTG 60
Qy      21 SerCyAluSgIySerGlyTyTrSerPheThrSerTyTrPleAlaTrpValArgGlnMet 40
Db      61 TCCTGCAAGGCTTCTGGTACTCATCTCACTGCTACTACATCAGCTGAGGTGGCCAGGCC 120
Qy      41 ProGlyLysGlyLeuGluTyTrMetGlyLeuIleTyTrProGlyAspSerAspThrLysTyTr 60
Db      121 CCCGACAGGCGCTTGAATGAGTGAAGTATTAATCTTAACAAATGAGTGTACTCTCTAC 180
Qy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyTr 80
Db      181 AACCAAGAAATTCAGAGACCGGCTGACATCTGCGACACTCCACCTCCACAGAGCTAC 240
Qy      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyTrPheCysAlaArgHisAsp 100

```

```
Db      241 ATGAGACCTCTCCTCGGCTCTGAGGACACCGCGCTTATTTACTGTGACGC----- 294
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      295 -----TCCACTATGATTACCAACTAT-----GTTATGAGCTACTGTGGGT 333
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121 GlnGlyThrLeuValThrValSerSer 129
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      334 CAAGGACCCCTGCTCAGCGCTCTCTCTCA 360

RESULT 14
US-11-297-317-12
; Sequence 12, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballedo Herrera
; APPLICANT: Jose M. Saldanha
; APPLICANT: Jose W. Hall
; APPLICANT: Bruce W. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Nucleotide sequence encoding amino acid sequence SEQ ID NO:10
US-11-297-317-12

Alignment Scores:
Pred. No.: 1.03e-33 Length: 354
Score: 358.50 Matches: 69
Percent Similarity: 72.1% Conservative: 24
Best Local Similarity: 53.5% Mismatches: 25
Query Match: 51.2% Indels: 11
DB: Gaps: 2
US-10-092-640-32 (1-129) x US-11-297-317-12 (1-354)

Qy      1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 20
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 CAGGTGCACCTGCTGTGAGTCCAGGAGCCGAAGTGAAGAAACCTGGGCTTCAGTGAAGCTG 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TCTGTCAAGGCTCTGTGATACACATTCACCTAATTATATATTCACCTGGGTGAAGCAGAG 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrIleTyr 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 CTTGTGACAGGCTCTGAATGATGATTTTAACTCTTACACATATATGATGATCAAGTAC 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 AATGAGAACTTCAAGGACGAGGCGCACATACGCAAAACAATCCATCAGCAGACGCTTAC 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 ATGAGACTCAGCAGCTGCGCTCTGAGGACACATGCGCTCTACTACTAGTCCAGA----- 294
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      295 -----TCAGGACCCCTATGCTG-----TTTGACACCTGGGGC 327
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121 GlnGlyThrLeuValThrValSerSer 129
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db      328 CAAGGACCAACGAGTCAACCGCTCTCTCA 354

RESULT 15
US-11-297-317-15
; Sequence 15, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballedo Herrera
; APPLICANT: Jose M. Saldanha
; APPLICANT: Jose W. Hall
; APPLICANT: Bruce W. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 8687
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Nucleotide sequence of the expression vector HCV-Hub-VHQ
; OTHER INFORMATION: (Complete DNA Sequence of a humanised heavy chain expression vect
; OTHER INFORMATION: or comprising SEQ ID NO:12 (VHQ) from 3921-4274)
US-11-297-317-15

Alignment Scores:
Pred. No.: 8.23e-32 Length: 8687
Score: 358.50 Matches: 69
Percent Similarity: 72.1% Conservative: 24
Best Local Similarity: 53.5% Mismatches: 25
Query Match: 51.2% Indels: 11
DB: Gaps: 2
US-10-092-640-32 (1-129) x US-11-297-317-15 (1-8687)

Qy      1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 20
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      3921 CAGGTGCACCTGCTGTGAGTCCAGGAGCCGAAGTGAAGAAACCTGGGCTTCAGTGAAGCTG 3980
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
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Db      4041 CTTGTGACAGGCTCTGAATGATGATTTTAACTCTTACACATCAGTCAAGTAC 4100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
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Db      4101 AATGAGAACTTCAAGGACGAGGCGCACATTACTGCAAAACAATCCATCAGCAGACCTTAC 4160
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      4161 ATGAGACTCAGCAGCTGCGCTCTGAGGACACATGCGCTCTACTACTAGTCCAGA----- 4214
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
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Db      4248 CAAGGACCAACGAGTCAACCGCTCTCTCA 4274

Search completed: May 25, 2006, 21:28:38
Job time : 25.425 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM proteoin - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:11:24 ; Search time 4225.86 Seconds
(without alignments)
2519.544 Million cell updates/sec

Title: US-10-092-640-36

Perfect score: 588
Sequence: 1 QSVLTPSPVSAARQKWT.....WDSLSGWVFGGSKTLVLG 111

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-YGAPOP=10 -YGAPEXT=0.5 -DLOP=6 -DLEXT=7

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2: gb_pat.*
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12: gb_hvg.*
13: gb_in.*
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15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	588	100.0	333	5 HSU36541	U36541 Human anti-
2	588	100.0	333	5 HSU38338	U38338 Human anti-
3	588	100.0	774	2 AR083879	AR083879 Sequence

4	588	100.0	774	2 AR278815	AR278815 Sequence
5	588	100.0	1509	8 AF516873	AF516873 Synthetic
6	580	98.6	333	5 HSU38345	U38345 Human anti-
7	579	98.5	333	5 HSU38342	U38342 Human anti-
8	578	98.3	333	5 HSU38346	U38346 Human anti-
9	575	97.8	333	5 HSU38335	U38335 Human anti-
10	573	97.4	333	5 HSU38341	U38341 Human anti-
11	569	96.8	333	5 HSU38336	U38336 Human anti-
12	568	96.6	333	5 HSU38343	U38343 Human anti-
13	567	96.4	333	5 HSU38347	U38347 Human anti-
14	562	95.6	333	5 HSU38340	U38340 Human anti-
15	558	94.9	333	5 HSU38344	U38344 Human anti-
16	556	94.6	333	5 HSU38337	U38337 Human anti-
17	556	94.6	332	5 HSA430768	HA430768 Homo sapi
18	542.5	92.3	336	5 HSU36537	U36537 Human anti-
19	536	91.2	333	5 HSU36538	U36538 Human anti-
20	536	91.2	333	5 HSU38339	U38339 Human anti-
21	535	91.0	333	5 HSU36536	U36536 Human anti-
22	527	89.6	387	5 HSVUMAB67	X54446 H.sapiens I
23	527	89.6	816	5 AB064150	AB064150 Homo sapi
24	526	89.5	781	5 AB064216	AB064216 Homo sapi
25	525	89.3	333	5 HSU36540	U36540 Human anti-
26	523	88.9	331	5 DQ187635	DQ187635 Homo sapi
27	523	88.9	744	8 AF487502	AF487502 Synthetic
28	522	88.8	333	5 HSU36539	U36539 Human anti-
29	521	88.6	331	5 DQ187610	DQ187610 Homo sapi
30	518	88.1	750	8 DQ250251	DQ250251 Synthetic
31	517	87.9	732	2 CQ0859620	CQ0859620 Sequence
32	517	87.9	744	8 AF487503	AF487503 Synthetic
33	516	87.8	740	2 CQ0832205	CQ0832205 Sequence
34	516	87.8	744	8 AF487505	AF487505 Synthetic
35	516	87.8	790	5 AB064206	AB064206 Homo sapi
36	516	87.8	831	5 AB064224	AB064224 Homo sapi
37	516	87.8	908	2 AR366275	AR366275 Sequence
38	515.5	87.7	729	8 DQ250225	DQ250225 Synthetic
39	515	87.6	342	5 HSA430759	HA430759 Homo sapi
40	514	87.4	333	5 HSA064038	AB064038 Homo sapi
41	514	87.4	706	2 CQ0832195	CQ0832195 Sequence
42	514	87.4	741	8 DQ201312	DQ201312 Synthetic
43	514	87.4	744	8 AF487507	AF487507 Synthetic
44	514	87.4	744	8 AF487508	AF487508 Synthetic
45	514	87.4	744	8 AF487509	AF487509 Synthetic

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V region mRNA,
partial cds.
U36541
ACCESSION U36541.1 GI:1145221
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Schier R., Bye J., Apell G., McCall A., Adams G.P., Weiner L.M. and
Marks J.D.
TITLE Isolation of high affinity monomeric Human anti-c-erbB-2 single
chain Fv using affinity driven selection
J. Mol. Biol. (1995) In press
REFERENCE
AUTHORS Schier R.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1995) Robert Schier, Anesthesia, University of
California at San Francisco, 1001 Potrero Avenue, San Francisco, CA
94110, USA
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ORIGIN

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Pred. No.: 6,45e-55 Length: 333
 Score: 588.00 Matches: 111
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0

US-10-092-640-36 (1-111) x HSU36541 (1-333)

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QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 61 TCCTGCTCTGGAAGCAGCGCTCCAACATTTGGGAATTAATTAATTAATTAATTAATTAAT 120
QY 41 ProGlyThrAlaProIleuLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro 60
DB 121 CCAGGAACAGCCCCCAACTCTCTCATCTATGTGCACACCAATCGGCCCCAGGGGTCCTCT 180
QY 61 AspArgPheSerGlySerIleSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
DB 181 GACCCATTCTTGGCTCCAAAGTCTGCGACCTCAGCTCCCTGGCCATTCAGTGGTTCCGG 240
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaAlaTTPAspAspSerIleuSerGlyTyrVal 100
DB 241 TCCGAGGATGAGCGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
QY 101 PheGlyGlyGlyThrIleuThrValIleuGly 111
DB 301 TTCGGCGGAGGAGCAACGCTGACCGTCTTAGGT 333

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RESULT 2
 HSU38338 333 bp mRNA linear PRI 02-OCT-1996
 LOCUS HsU38338
 DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,
 clone C6PM4.
 ACCESSION U38338.1 GI:1145337
 VERSION U38338.1
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 333)
 Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
 Marks,J.D.
 Identification of functional and structural amino-acid residues by
 paraimmunious mutagenesis
 JOURNAL Gene 169 (2), 147-155 (1996)
 PUBMED 8647439
 REFERENCE 2 (bases 1 to 333)
 Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
 Marks,J.D.
 TITLE Direct Submission

JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
 Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
 FEATURES location/Qualifiers
 source 1..333

CDS

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ORIGIN

Alignment Scores:

Pred. No.: 6,45e-55 Length: 333
 Score: 588.00 Matches: 111
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
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US-10-092-640-36 (1-111) x HSU38338 (1-333)

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QY 61 AspArgPheSerGlySerIleSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
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QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaAlaTTPAspAspSerIleuSerGlyTyrVal 100
DB 241 TCCGAGGATGAGCGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
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DB 301 TTCGGCGGAGGAGCAACGCTGACCGTCTTAGGT 333

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RESULT 3
 AR083879 774 bp DNA linear PAT 01-SEP-2000
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 DEFINITION Sequence 4 from patent US 5977322.
 ACCESSION AR083879
 VERSION AR083879.1 GI:10010650
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 1 (bases 1 to 774)
 Marks,J.D. and Schier,R.
 High affinity human antibodies to tumor antigens
 JOURNAL Patent: US 5977322-A 4 02-NOV-1999;
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 Score: 588.00 Matches: 111
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 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x AR083879 (1-774)

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 Qy 21 SerCysSerGlySerSerSerSerAniIleGlyAsnAsnTrpValSerTrpTrpGlnGlnIleu 40
 Db 493 TCGTCTCTGGAAGCAGCTCCACATGGGAATTAATATATCTGTTACAGCAGACTC 552
 Qy 41 ProGlyThrAlaProIleuLeuIleTyRGlyVhiThsAsnArpProIleGlyValPro 60
 Db 553 CCGAGAACAGCCCCCAACTCCCTCATCTATGTCACACCAATCGGCCCGAGGGGTCCTC 612
 Qy 61 AspArgPheSerGlySerIleYserIleThsSerAlaSerLeuAlaIleSerGlyPheArg 80
 Db 613 GACCGATTCTGTGGCTCCAAGTCTGGACCTCCTCCGTCATCAGTGGTTCCGG 672
 Qy 81 SerGluAspGluAlaAspTrpTrpCysAlaIleTrpAspAspSerLeuSerGlyTrpVal 100
 Db 673 TCCGAGATGAGGCTGATTAATTAATCTGACGATGGAGATGACAGCTGAGTGGTG 732
 Qy 101 PheGlyGlyGlyThrIleuThrValIleuGly 111
 Db 733 TTGGCGGAGGAGCAAGCTGACCGTCTTAGGT 765

RESULT 4
 AR278815 774 bp DNA linear PAT 10-APR-2003
 LOCUS Sequence 4 from patent US 6512097.
 DEFINITION AR278815
 ACCESSION AR278815
 VERSION AR278815.1 GI:29713203
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 774)
 AUTHORS Marks, J.D. and Schlier, R.
 TITLE High affinity human antibodies to tumor antigens
 JOURNAL Patent: US 6512097-A 4 28-JUN-2003
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 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x AR278815 (1-774)

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 Db 433 CAGTCTGTGTGAAGCGAGCCGCTCAGTCTGCGGCCCGACGACGAGAGGTCAACATC 492
 Qy 21 SerCysSerGlySerSerSerSerAniIleGlyAsnAsnTrpValSerTrpTrpGlnGlnIleu 40
 Db 493 TCGTCTCTGGAAGCAGCTCCACATGGGAATTAATATATCTGTTACAGCAGACTC 552

Qy 41 ProGlyThrAlaProIleuLeuIleTyRGlyVhiThsAsnArpProIleGlyValPro 60
 Db 553 CCGAGAACAGCCCCCAACTCCCTCATCTATGTCACACCAATCGGCCCGAGGGGTCCTC 612
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 Db 733 TTGGCGGAGGAGCAAGCTGACCGTCTTAGGT 765

RESULT 5
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 LOCUS Synthetic construct membrane-acting immunotoxin fusion protein
 DEFINITION AF516873
 ACCESSION AF516873
 VERSION AF516873.1 GI:31324248
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 1509)
 AUTHORS Gurkan, C. and Ellar, D.J.
 TITLE Design and construction of membrane-acting immunotoxins based on the Bacillus thuringiensis delta-endotoxin Cyt2Aa1 for expression in Pichia pastoris
 Med. Microbiol. Immunol. (Berl.) 189, 37-37 (2000)
 JOURNAL 2 (bases 1 to 1509)
 REFERENCE Gurkan, C. and Ellar, D.J.
 AUTHORS Expression in Pichia pastoris and purification of a membrane-acting immunotoxin based on a synthetic gene coding for the Bacillus thuringiensis Cyt2Aa1 toxin
 Protein Expr. Purif. 29 (1), 103-116 (2003)
 JOURNAL 3 (bases 1 to 1509)
 REFERENCE Gurkan, C. and Ellar, D.J.
 AUTHORS Expression of the Bacillus thuringiensis Cyt2Aa1 toxin in Pichia pastoris using a synthetic gene construct
 Biotechnol. Appl. Biochem. 38 (Pt 1), 25-33 (2003)
 JOURNAL 4 (bases 1 to 1509)
 REFERENCE Gurkan, C., Ellar, D.J. and Marks, J.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAY-2002) Department of Biochemistry, University of Cambridge, 80 Tennis Court Road, Old Addenbrooke's Site, Cambridge CB2 1GA, England
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 source
 CDS

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DB:	8
US-10-092-640-36 (1-111) x AFS16873 (1-1509)	
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	Matches: 111
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

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Oy	21 SerCysSerGlySerSerSerSerAsnIleGlyAsnAsnTyrValSerTyrGlnGlnIleu	40
Db	508 TCTCTGCTTGGAAAGACGCTCCAACTATGGGAATTAATGATCTCGTAGCACGACGCTC	567
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Db	568 CCAGGAACAGCCCCCAAACTCTCATCTATGTCATCACCAATTCGGCCGCGAGGGGTCTCT	627
Oy	61 AsparGlnPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg	80
Db	628 GACCGATTCTCTGGGCTCCCAAGCTCTGGACCTCAGGCTCCCTGGCCATCAGTGGGTTCGCG	687
Oy	81 SerGlnAspGlnAlaAspTyrTyrCysAlaAlaIATPAspAspSerIleuSerGlyTyrVal	100
Db	688 TCCGAGGATGAGGCTGATTATTACTGTGGAGCATGGGATGACAGCCTGATGTGGTGGGTG	747
Oy	101 PheGlyGlyGlyThrIleLeuThrValLeuGly	111
Db	748 TTCGGCGGAGGAGCAACGCTGACCGTCTTAGGT	780

RESULT 6	HSU38345	LOCUS DEFINITION
333 bp	HSU38345	Human anti-C-erbB-2 immunoglobulin light chain V mRNA, partial cds.
linear		Clone C6PM1.1.
PRI 02-OCT-1996		

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	U38345 U38345.1 GI:1145351 . Homo sapiens (human)
REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 333) Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.
TITLE	Identification of functional and structural amino-acid residues by parisonous mutagenesis
JOURNAL PUBMED	Gene 169 (2) , 147-155 (1996) 8647438
REFERENCE AUTHORS	2 (bases 1 to 333) Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.

TITLE	Direct Submission
JOURNAL	Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
FEATURES	Location/Qualifiers
SOURCE	1. .333

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[illegible]

US-10-092-640-36 (1-111) X HSU38345 (1-333)

[illegible]

RESULT 7	LOCUS	DEFINITION
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HSU38342	Human anti-c-erbB-2 immunoglobulin light chain V	mRNA, partial cds
	clone C6PM8.	

ACCESSION	U38342
VERSION	U38342.1
KEYWORDS	GI:1145345
SOURCE	
ORGANISM	Homo sapiens (human)
	Homo sapiens
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REFERENCE	1 (bases 1 to 333)
AUTHORS	Scherer,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.
TITLE	Identification of functional and structural amino-acid residues by
JOURNAL	parisiomous mutagenesis
	Gene 169 (2), 147-155 (1996)

PUBMED 8647439
REFERENCE 2 (bases 1 to 333)
AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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 QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
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 DB 121 CCAAGAACAGCCCCCAACTCTCATCTATGTCACACCAATCGCCCGAGGGGTCCCT 180
 QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 DB 181 GACCGATTCTCTGGCTCCAGTCTGGCACCTCAGCTCCCTGGCCATCAGTGGGTTCCGG 240
 QY 81 SerGluAspGluAlaAspTyrrTyrcysAlaAlaITrpAspAspSerLeuSerGlyTrpVal 100
 DB 241 TCCGAGATGAGGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
 QY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
 DB 301 TTCCGCGGAGGAGCAAGCTGACCGTCTAAGT 333
RESULT 8
 HSU38346 333 bp mRNA linear PRI 02-OCT-1996
 LOCUS Human anti-c-erbB-2 immunoglobulin light chain v mRNA, partial cds,
 DEFINITION clone CGPM12.
 ACCESSION U38346.1 GI:1145353
 VERSION U38346.1
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
REFERENCE 1 (bases 1 to 333)
AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and

Marks,J.D.
TITLE Identification of functional and structural amino-acid residues by
 parsimonious mutagenesis
JOURNAL Gene 169 (2), 147-155 (1996)
PUBMED 8647439
REFERENCE 2 (bases 1 to 333)
AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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 QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
 DB 61 TCCTGCTGTGAGAGCAGCTCAACATGTGTAATATATATATATATATATATATATATAT 120
 QY 41 ProGlyThrAlaProIysLeuLeuIleTyrglyHisThrAsnArgProAlaGlyValPro 60
 DB 121 CCAAGAACAGCCCCCAACTCTCATCTATGTCACACCAATCGCCCGAGGGGTCCCT 180
 QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 DB 181 GACCGATTCTCTGGCTCCAGTCTGGCACCTCAGCTCCCTGGCCATCAGTGGGTTCCGG 240
 QY 81 SerGluAspGluAlaAspTyrrTyrcysAlaAlaITrpAspAspSerLeuSerGlyTrpVal 100
 DB 241 TCCGAGATGAGGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
 QY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
 DB 301 TTCCGCGGAGGAGCAAGCTGACCGTCTAAGT 333
RESULT 9
 HSU38335 333 bp mRNA linear PRI 02-OCT-1996
 LOCUS Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,
 DEFINITION clone CGPM1.
 ACCESSION U38335.1 GI:1145331
 VERSION U38335.1
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
REFERENCE	Hominidae, Homo.
AUTHORS	1 (bases 1 to 333)
TITLE	Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D. Identification of functional and structural amino-acid residues by parsimonious mutagenesis
JOURNAL	Gene 169 (2), 147-155 (1996)
PUBMED	8647439
REFERENCES	2 (bases 1 to 333) Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D. Direct Submision Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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Oy	21 SerCysserGylSerSeSerAsmlleglvsaNsantYrvalSetTrPyTnglndeu 40
Dd	61 TCctgcTtcTGAGAagCaGCTCCAACA TGATAATTAtTArtCTGSgtTaCcAcAGCTC 120
Oy	41 ProglyThrAlaprolvslenleunlleTyglqlyshlrAsanaRproalaglvaIPro 60
Dd	121 CCAGGAACAGCCCCCAAACCCTCATCTATNGTCACACCAATCGGCCGCGAGGGGTCCCCT 180
Oy	61 AsparghPheSerGylSerLySerGylShSerlaserLeuaialieSerGylPhenArg 80
Dd	181 GAACGaTTCTTGgCTccaagtCTggCaCCTcaGCTCCtCGGCCATatAGTGGgtTCGGG 240
Oy	81 SerGluaSpGiualaasPTyrTYrcysAlaalatrpaSepaSerLeusergilyTpivaI 100
Dd	241 TCCgaGATGaGGCTgatTTattACTGtGCacAanRGaTGATAdactttGtgtGGGTG 300
Oy	101 PheglvglylglyThntvlsvleuthrvallengely 111
Dd	301 TTcgCGCGAGGAGAACCAAGCTGACCGTCCtaAGT 333
RESULT 10	
LOCUS	HSU38341 333 bp mRNA linear PRI 02-OCT-1996
DEFINITION	Human anti-C-erbB-2 immunoglobulin light chain V mRNA, partial cds,
ACCESSION	U38341 GI:1145343
VERSION	U38341.1

KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 333)		
AUTHORS	Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.		
TITLE	Identification of functional and structural amino-acid residues by parsimonious mutagenesis		
JOURNAL	Gene 169 (2), 147-155 (1996)		
PUBMED	8647439		
REFERENCE	2 (bases 1 to 333)		
AUTHORS	Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-OCT-1995) Robert Schier, Anestesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA		
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US-10-092-640-36 (1-111) x HSU38336 (1-333)			
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Db	1	CAGTCTGTGTGAAGCAGCCGCCCTCACTGCTCTCGGCCCCAGACAGAAAGTCAACATC	60
Oy	21	SerCysSerGlySerSerSerSerAsnIleGlyAsnAsnTyValSerTyrGlnGlnLeu	40
Db	61	TCTCGCTCTGGAAACACCTCCAACTATGTAATATATATCTCTGTAACCAAGCACTC	120
Oy	41	ProGlyThrIaIaProLysLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro	60
Db	121	CCAGAAACAGCCCCCAACTCTCTCATTTATAGTGTGCACCAATGCGCCCGAGGGGTCTT	180
Oy	61	AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg	80
Db	181	GACCGATTCTCTGTGCTCCAAAGTGGGACCTCAAGCTCCTGTGGCCATCAGTGGGTTCCGG	240
Oy	81	SerGluAspGluAlaAspTyrTyrCysAlaAlaIaTrpAspAspSerLeuSerGlyTyrVal	100
Db	241	TCCAGAGATAGAGCTGATTATTTACTGTGACAGCAATGGGATCATTTGTGTGGTTGGGTG	300
Oy	101	PheGlyGlyGlyThrLysLeuThrValIleGly	111
Db	301	TTCCGCGGAGGAGCAACCACTGACCGTCTTAGT	333
RESULT 11			
LOCUS	HSU38336	333 bp	mRNA linear PRI 02-OCT-1996

DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds, clone C6PM2.

ACCESSION U38336

VERSION U38336.1 GI:1145333

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 333)

AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.

TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis

JOURNAL Gene 169 (2), 147-155 (1996)

PubMed 8647439

REFERENCE 2 (bases 1 to 333)

AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.

TITLE Direct Submission

JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA

FEATURES

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ORIGIN

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Pred. No.:	7,688-53	Length:	333
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US-10-092-640-36 (1-111) x HSU38336 (1-333)

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DB 181 GACCGATTCTCTGGCTCCCAAGTCGACCTCAGCTCCCTGCGCATCAGTGGGTTCCGG 240

QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaTrpAspAspSerLeuSerglyTrpVal 100

DB 241 TCCGAGGATGAGGCTATTAATTAATCTGTGCGCATGGAGATGATGCTGAGACTGTGGGTG 300

QY 101 PheGlyGlyGlyThyIleSleuThrValIleuGly 111

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RESULT 12

HSU38343

LOCUS 333 bp mRNA linear PRI 02-OCT-1996

DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds, clone C6PM9.

ACCESSION U38343

VERSION U38343.1 GI:1145347

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 333)

AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.

TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis

JOURNAL Gene 169 (2), 147-155 (1996)

PubMed 8647439

REFERENCE 2 (bases 1 to 333)

AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.

TITLE Direct Submission

JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA

FEATURES

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ORIGIN

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US-10-092-640-36 (1-111) x HSU38343 (1-333)

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DB 1 CAGTCTGTGTTGACGACGCGCCCTCAGTGTGCGGCCCAAGACAGAGTCACATC 60

QY 21 SerCySeSerGlySeSerSerAenIleGlyAmaAsnTyValSerTrpTyrgInGlnIleu 40

DB 61 TCTGTCTCTGGAAGCGCTCCCAAGTCATGTAAGAAATTATGTAATCCGTAACGACGCTC 120

QY 41 ProGlyThraAlaProLySleuLeuIleTyrgIyHisThraAsnArgProIaGlyValPro 60

DB 121 CCAAGAAACGCCCCCAACTCCTCATCTATGTCACACCAATGCGCCCGAGGGGTCCT 180

QY 61 AAPaGPhSeSerGlySeLySerSerglyThrSerAlaSerLeuAlaIleSerglyPheArg 80

DB 181 GACCGATTCTCTGGCTCCCAAGTCGACCTCAGCTCCCTGCGCATCAGTGGGTTCCGG 240

QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaTrpAspAspSerLeuSerglyTrpVal 100

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Qy      101 PheGlyGlyGlyThrIysLeuThrValIleuGly 111
Db      301 TTCGGCGAGGAGCAAGCTGACCGCTCTAGGT 333

RESULT 13
LOCUS    HSU38347
DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,
            clone C6PM13.
ACCESSION U38347
VERSION   U38347.1 GI:1145355
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
REFERENCE Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
AUTHORS   Marks,J.D.
TITLE     Identification of functional and structural amino-acid residues by
JOURNAL   Gene 169 (2), 147-155 (1996)
PUBMED    8647439
REFERENCE 2 (bases 1 to 333)
AUTHORS   Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
            Marks,J.D.
TITLE     Direct Submission
JOURNAL   Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
            Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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Alignment Scores:
Pred. No.: 1,27e-52 Length: 333
Score: 567.00 Matches: 107
Percent Similarity: 98.2% Conservative: 2
Best Local Similarity: 96.4% Mismatches: 2
Query Match: 96.4% Indels: 0
DB: 5 Gaps: 0

US-10-092-640-36 (1-111) x HSU38347 (1-333)

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Qy      21 SerCysSerGlySerSerSerSerAniIleGlyAsnAsnTyrValSerTyrTyrGlnGlnLeu 40
Db      61 TCTCTGCTCTGGAGAGCGCTCCAACTGGTAAATAATTACGTATCCCTGGTACACGACGCTC 120

Qy      41 ProGlyThrAlaProIysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
Db      121 CAGGAGACAGCCCCAAACTCCTCATCTATGTGTCACACCAATCGGCCCGCAGGAGTCCCT 180

Qy      61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
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Qy      81 SerGluAepGluAlaAspTyrTyrCysAlaAlaITrpaAspSerLeuSerGlyTrrVal 100
Db      241 TCCGAGGATAGAGCGCATATTATTCGTGCAGATGGAGTATTTCTTGTCTGGTTGGTG 300

Qy      101 PheGlyGlyGlyThrIysLeuThrValIleuGly 111
Db      301 TTCGGCGAGGAGCAAGCTGACCGCTCTAGGT 333

RESULT 14
LOCUS    HSU38340
DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,
            clone C6PM6.
ACCESSION U38340
VERSION   U38340.1 GI:1145341
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
REFERENCE Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
AUTHORS   Marks,J.D.
TITLE     Identification of functional and structural amino-acid residues by
JOURNAL   Gene 169 (2), 147-155 (1996)
PUBMED    8647439
REFERENCE 2 (bases 1 to 333)
AUTHORS   Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
            Marks,J.D.
TITLE     Direct Submission
JOURNAL   Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
            Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 4.47e-52 Length: 333
Score: 562.00 Matches: 107
Percent Similarity: 97.3% Conservative: 1
Best Local Similarity: 96.4% Mismatches: 3
Query Match: 95.6% Indels: 0
DB: 5 Gaps: 0

US-10-092-640-36 (1-111) x HSU38340 (1-333)

Qy      1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIle 20
Db      1 CAGTCTGTGTTGACGAGCGCCCTCAGTGTCTGCGGCCCGAGAGCAGAAAGTCACAAG 60

Qy      21 SerCysSerGlySerSerSerSerAniIleGlyAsnAsnTyrValSerTyrTyrGlnGlnLeu 40
Db      61 TCTCTGCTCTGGAGAGCGCTCCAACTGGTAAATAATTACGTATCCCTGGTACACGACGCTC 120

Qy      41 ProGlyThrAlaProIysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
Db      121 CAGGAGACAGCCCCAAACTCCTCATCTATGTGTCACACCAATCGGCCCGCAGGAGTCCCT 180

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QY      61  ASPARGPHESEGLYSERLYSERGLYTHRSEALASERLEUALLESERGLYPHEARG 80
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DB      181  GACCGATTCTCTGCTCCAGAGTGTGGACCTGACCTCCCTGCTATCACTGGGTTCCGG 240
QY      81  SERGLUASPGLUALAAPTLYTYRCYSAALALATPASPAPSERLEUSERGLYTRIPVAL 100
      |||
DB      241  TCCGAGATGAGGCTGATTATTACTGTGCGACATGGATTATCTTTGTCTGGTTGGGTG 300
QY      101  PHEGLYGLYGLYTHRLYSLEUTHRVALLLEUGLY 111
      |||
DB      301  TTCGGCGGAGGAGCAAGCTGACCGTCTAGGT 333

RESULT 15
HSU38344      333 bp      mRNA      linear      PRI 02-OCT-1996
LOCUS      Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,
DEFINITION      clone C6PM10.
ACCESSION      U38344
VERSION      U38344.1  GI:1145349
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 333)
AUTHORS      Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
      Marks, J.D.
      Identification of functional and structural amino-acid residues by
      parimonious mutagenesis
      Gene 169 (2), 147-155 (1996)
      8647439
      2 (bases 1 to 333)
      Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
      Marks, J.D.
      Direct Submission
      Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
      Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
      Location/Qualifiers
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      /protein_id="AAB09654.1"
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      /translation="OSVLTQPPSVSAPOQKVTISCGSSSNIGNDVMYSWYOQLPQTA
      PKLLIYGHTRNPAGVDPDRSGSKTSASLASISGRSEDEADYYCAPMDASQYGMVFG
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ORIGIN

Alignment Scores:
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Score:      558.00      Matches:      106
Percent Similarity:      96.4%      Conservative:      1
Best Local Similarity:      95.5%      Mismatches:      4
Query Match:      94.9%      Indels:      0
DB:      5      Gaps:      0

US-10-092-640-36 (1-111) X HSU38344 (1-333)

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QY      21  SERCYSESGLYSERSESERSEANILEGLYASNAANTYVALSERTRPYRGINGINLEU 40
      |||
DB      61  TCTGTCTCTGGAAGCAAGCTCCAACTTGGGGAATATTATGTATCTGTGTAACGACGCTC 120

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QY      41  PROGLYTHRALAPROLYSLEULEUILETYRGLYHIETHRASNAKPPROALAGLYVALPRO 60
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QY      61  ASPARGPHESEGLYSERLYSERGLYTHRSEALASERLEUALLESERGLYPHEARG 80
      |||
DB      181  GACCGATTCTCTGCTCCAGAGTGTGGACCTGACCTCCCTGSCCATCACTGGGTTCCGG 240
QY      81  SERGLUASPGLUALAAPTLYTYRCYSAALALATPASPAPSERLEUSERGLYTRIPVAL 100
      |||
DB      241  TCCGAGATGAGGCTGATTATTACTGTGCGCCGCTGGGAGCGCTCCCAAGTACGGGTGGGTG 300
QY      101  PHEGLYGLYGLYTHRLYSLEUTHRVALLLEUGLY 111
      |||
DB      301  TTCGGCGGAGGAGCAAGCTGACCGTCTAGGT 333

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Search completed: May 25, 2006, 19:00:43
 Job time : 4227.86 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:10:39 ; Search time 473.138 Seconds
(without alignments)
2453.577 Million cell updates/sec

Title: US-10-092-640-36

Perfect score: 588
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Ygapop	10.0 ,	Ygapext 0.5
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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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-UNITS-bits -START=1 -END=1 -MATRIX=bls00002 -TRANS=numa40.cdi -LIST=45
-DOCLALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=p10 -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h5h
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8:   geneseqnr2003bs:*
9:   geneseqnr2003bs:*
10:  geneseqnr2003cs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	DESCRIPTION
1	588	100.0	765	6	AAD32664	Aad32664 Chimeric
2	588	100.0	774	2	AAT50787	Aat50787 C6 human
3	566	96.3	807	6	AAD32665	Aad32665 Chimeric

4	566	96.3	846	6	AA032666	Ad32666 Chimeric
5	566	96.3	856	6	AA032667	Ad32667 Chimeric
6	566	96.3	873	6	AA032669	Ad32669 Chimeric
7	566	96.3	888	6	AA032668	Ad32668 Chimeric
8	553	94.0	333	12	Adm98169	Adm98169 Anti-apo
9	545	92.7	333	12	Adm00519	Adm00519 Anti-apo
10	545	92.7	333	12	Adm98139	Adm98139 Anti-apo
11	536	91.2	333	12	Adm98163	Adm98163 Anti-apo
12	533.5	90.7	336	12	Adm00515	Adm00515 Anti-apo
13	533.5	90.7	336	12	Adm98135	Adm98135 Anti-apo
14	531	90.3	333	12	Adm98167	Adm98167 Anti-apo
15	529	90.0	333	12	Adm00521	Adm00521 Anti-apo
16	529	90.0	333	12	Adm98141	Adm98141 Anti-apo
17	527	89.6	333	12	Adm98171	Adm98171 Anti-apo
18	525	89.3	333	12	Adm00523	Adm00523 Anti-apo
19	525	89.3	333	12	Adm98143	Adm98143 Anti-apo
20	524.5	89.2	336	12	Adm98161	Adm98161 Anti-apo
21	521	88.6	333	12	Adm98165	Adm98165 Anti-apo
22	520	88.4	333	12	Adm98155	Adm98155 Anti-apo
23	517	87.9	732	13	AdS09325	AdS09325 Human G
24	516	87.8	333	12	Adm00525	Adm00525 Anti-apo
25	516	87.8	333	12	Adm98145	Adm98145 Anti-apo
26	516	87.8	740	13	AdR28123	AdR28123 Polyucel
27	516	87.8	744	14	AdV85637	AdV85637 Anti-hum
28	516	87.8	908	6	ABa1388	ABa1388 Anti-Baci
29	516	87.8	908	12	AdI39011	AdI39011 Human CD
30	514	87.4	706	13	AdR28113	AdR28113 Polyucel
31	513	87.2	2635	11	ACN92379	ACN92379 Breast C
32	511	86.9	411	14	AdW04702	AdW04702 PAP-A I
33	510	86.7	333	12	Adm98157	Adm98157 Anti-apo
34	510	86.7	333	14	AdZ66173	AdZ66173 CDNA enc
35	510	86.7	333	15	AEF94036	AEF94036 Human ant
36	510	86.7	354	14	AdV50080	AdV50080 Endothel
37	510	86.7	762	14	AdE12496	AdE12496 Anti-Nog
38	508	86.4	337	5	AAH68613	AAH68613 Human ant
39	508	86.4	337	15	ACD45337	ACD45337 Anti-Rh(D
40	508	86.4	337	9	AEER74500	AEER74500 Anti-Rh
41	508	86.4	726	2	AAH66937	AAH66937 Antibody
42	508	86.4	726	2	AAH66936	AAH66936 Antibody
43	507	86.2	378	12	Adm98159	Adm98159 Anti-apo
44	505.5	86.0	764	10	AdR81314	AdR81314 F8 scFv
45	504	85.7	333	2	AAV72226	AAV72226 Human ant

XX	RESULT 1	
XX	AAD32664	
XX	AAD32664 standard; DNA; 765 BP.	
XX	AAD32664;	
XX		
DT	29-AUG-2003 (revised)	
DT	18-JUN-2002 (first entry)	
XX		
DE	Chimeric SCBP C6.5 sfv DNA.	
XX		
KW	Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;	
KW	nucleic acid-binding moiety; NAM; lipid-associating moiety; LAM;	
KW	gene therapy; targeted gene delivery; human; murine; chimeric; ds.	
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OS	Homo sapiens.	
OS	Mus sp.	
OS	Chimeric.	
XX		
XX	Key	Location/Qualifiers
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FT		/product= "Chimeric SCBP C6.5 sfv protein"
FT		/note= "CDS does not include start and stop codon"
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XX		
NN	W0200200914-A2.	

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XX 03-JAN-2002.
PD 25-JUN-2001; 2001WO-US020182.
XX 23-JUN-2000; 2000US-0213653P.
XX (HUST/) HUSTON J S.
PA (WILS/) WILS P.
PA (QUAN/) QUAN Z.
PA (LAUR/) LAURENT O.
PA (MARASCO/) MARASCO W A.
PA (SCHE/) SCHERMAN D.
XX Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
DR WPI; 2002-268789/31.
DR P-PSDB; AAE20407.
XX
XX Gene-delivery compound for targeted gene delivery, comprises single-chain
PT binding polypeptide having effector segment with cysteinyl residue and
PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
PT residue.
XX
XX Disclosure; Fig 4; 96pp; English.
XX
XX The invention relates to gene-delivery compound comprising a single-chain
CC binding polypeptide (SCBP) having at least one effector segment having a
CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
CC compound is useful for targeted gene delivery for treating diseases by
CC gene therapy. The present sequence is chimeric SCBP C6.5 sFv DNA
CC comprising human and murine sequences. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 765 BP; 155 A; 217 C; 227 G; 166 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.56e-47 Length: 765
Score: 588.00 Matches: 111
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-092-640-36 (1-111) x AAD32664 (1-765)
QY 1 GlnSerValLeuThrGlnProSerValSerAlaAlaProGlyGlnIysValThrIle 20
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QY 21 SerCysSerGlySerSerSerSerAniIegIysAnSerTrpValSerTrpTyrGlnIleu 40
DB 493 TCTCTGCTCTGGAAGCAGCTCCAAATGGGAATTAATTAATGATCCGTACGACGAGCTC 552
QY 41 ProGlyThrAlaProIysIleuIleTyrGlyVHisThrAspArgProIaGlyValPro 60
DB 553 CCAAGGAACGCCCCCAACTCCCATCTATGGTCACACCAATCGGCCCCAGAGGGCTCCCT 612
QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
DB 613 GACCGATTCTCTGGCTCCAAAGTCTGGCACTCAAGCTCCCTGGCCATCAGTGGTTCCGG 672
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTyrAspAspSerIleuSerGlyTyrVal 100
DB 673 TCCGAGGATGAGGCTGATTAATTAATGTCAGCATGGATGACAGCTGAGTGGTGGTG 732
QY 101 PheGlyGlyGlyThrIysIleuThrValIleGly 111
DB 733 TTGGGGGAGGAGCAAGCTGACCGTCTAGGT 765

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ID AAT50787 standard; DNA; 774 BP.
XX AC AAT50787;
XX 23-SEP-1997 (first entry)
XX C6 human sFv antibody C6.5 encoding DNA.
XX Tumour; immune response; cytotoxin; carcinoma; breast cancer; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 1..774
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FT /product= "Antibody_C6.5"
FT /transl_except= (pos: 181..183, aa: Ser)
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XX
XX WO9700271-A1.
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XX 03-JAN-1997.
XX
XX 13-JUN-1996; 96WO-US010287.
XX
XX 14-JUN-1995; 95US-0000238P.
XX 15-JUN-1995; 95US-0000250P.
XX
XX (BEGC ) UNIV CALIFORNIA.
XX
XX Marks JD, Schier R;
XX
XX WPI; 1997-077488/07.
XX P-PSDB; AAW08487.
XX
XX New C6 human antibody binding specifically to c-erbB-2 - useful for
PT treatment and diagnosis of tumours, with reduced risk of generating
PT immune response.
XX
XX Claim 4; Fig 1; 117pp; English.
XX
XX The present sequence encodes a C6 human antibody C6.5, that binds
CC specifically to c-erbB-2. A chimeric molecule that binds specifically to
CC tumour cells carrying c-erbB-2 consists of an effector compound attached
CC to a C6 human antibody, e.g. C6.5. If the effector compound is a
CC cytotoxin the chimeric molecule can be used to inhibit growth of c-erbB-2
CC positive tumours (especially breast and other carcinomas). If the
CC effector compound is a label the chimeric molecule can be used to detect
CC such cells, including in vivo localisation. The antibody can also be used
CC for diagnosis/localisation, in vivo or in vitro, especially by
CC immunoassay. The nucleic acid encoding the antibody, and a nucleic acid
CC encoding a single chain polypeptide with the binding specificity of the
CC antibody and comprising the binding portions of variable regions of light
CC and heavy chains of the antibody, joined by a linker, can be used to
CC produce recombinant proteins by standard methods. Unlike known anti-c-
CC erbB-2 antibodies, C6 antibodies are fully human, so should elicit
CC little, if any, immunogenic response
XX
SQ Sequence 774 BP; 156 A; 222 C; 230 G; 166 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.56e-47 Length: 774
Score: 588.00 Matches: 111
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-092-640-36 (1-111) x AAT50787 (1-774)
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Db      433 CAGTCTGTGTGACGACGCCCTCAGTCTGCGGCCCGACAGAGAGTCACCATC 492
Qy      21 SerCySerGlySerSerSerAanIegLyAsnAsnTyValSerTPYrGInGlnLeu 40
Db      493 TCCTGCTCTGGAGAGCGCTCCACATGGGAATATATATCTGCTGATCCAGCAGCTC 552
Qy      41 ProGlyThAlAProLyLeuLeuIleTyGlyHisThAsnArpProaIagIyValPro 60
Db      553 CCAGGAACAGCCCCCAAACTCCATCTATAGTCACACCAATCGGCCCGAGGGGTCCCT 612
Qy      61 AspArgPheSerGlySerLySerGlyThSerAlaSerLeuAlaIleSerGlyPheArg 80
Db      613 GACCGATTCTCTGCTCCAGCTGCGACCTCCCTGCGCATCAGTGGGTCCGG 672
Qy      81 SerGluAspGluAlaAspTyTyTyCyAlaAlaATrpaSpsAspSerLeuSerGlyTyrVal 100
Db      673 TCCGAGGATGAGGCTGATTTATTACTGTGCAGCATGGGATGACAGCTGATGGTGGGTG 732
Qy      101 PheGlyGlyGlyThTyrsLeuThrValLeuGly 111
Db      733 TTCGGCGAGGAGCAACGCTGACCGTCTAGGT 765

RESULT 3
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ID      AAD32665 standard; DNA; 807 BP.
AC      AAD32665;
DT      29-AUG-2003 (revised)
DT      18-JUN-2002 (first entry)
XX      Chimeric SCBP C6ML3-9 sfv' DNA.
DE      Chimeric SCBP C6ML3-9 sfv' DNA.
XX      Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
KM      nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
KW      gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX      Homo sapiens.
OS      Mus sp.
OS      Chimeric.
XX      Key Location/Qualifiers
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XX      AC AAD32666;
XX      DT 29-AUG-2003 (revised)
XX      DT 18-JUN-2002 (first entry)
XX      DE Chimeric SCBP C6ML-3-9sfv'-L1-KDEL DNA.
XX      DE Chimeric SCBP C6ML-3-9sfv'-L1-KDEL DNA.
XX      KM Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
XX      KM nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
XX      KW gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX      OS Homo sapiens.
XX      OS Mus sp.
XX      OS Chimeric.
XX      PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
XX      DR WPI; 2002-268789/31.
XX      PT Gene-delivery compound for targeted gene delivery, comprises single-chain
XX      PT binding polypeptide having effector segment with cysteinyl residue and
XX      PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
XX      PT residue.

```

```

PS      Disclosure; Fig 6; 96pp; English.
XX      CC The invention relates to gene-delivery compound comprising a single-chain
XX      CC binding polypeptide (SCBP) having at least one effector segment having a
XX      CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
XX      CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
XX      CC compound is useful for targeted gene delivery for treating diseases by
XX      CC gene therapy. The present sequence is chimeric SCBP C6ML3-9 sfv' DNA
XX      CC comprising human and murine sequences. (Updated on 29-AUG-2003 to
XX      CC standardise OS field)
XX      SQ Sequence 807 BP; 160 A; 240 C; 237 G; 170 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,11e-45 Length: 807
Score: 566.00 Matches: 107
Percent Similarity: 98.2% Conservative: 2
Best Local Similarity: 96.4% Mismatches: 2
Query Match: 96.3% Indels: 0
DB: 6 Gaps: 0

US-10-092-640-36 (1-111) x AAD32665 (1-807)
Qy      1 GlnSerValIleuThrgInPProSerValSerAlaIaProGlyGlnIyValThrIle 20
Db      433 CAGTCTGTGTGACGACGCCCTCAGTCTGCGGCCCGACAGAGAGTCACCATC 492
Qy      21 SerCySerGlySerSerSerAanIegLyAsnAsnTyValSerTPYrGInGlnLeu 40
Db      493 TCCTGCTCTGGAGAGCGCTCCACATGGGAATATATATCTGCTGATCCAGCAGCTC 552
Qy      41 ProGlyThAlAProLyLeuLeuIleTyGlyHisThAsnArpProaIagIyValPro 60
Db      553 CCAGGAACAGCCCCCAAACTCCATCTATAGTCACACCAATCGGCCCGAGGGGTCCCT 612
Qy      61 AspArgPheSerGlySerLySerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db      613 GACCGATTCTCTGCTCCAGCTGCGACCTCCCTGCGCATCAGTGGGTCCGG 672
Qy      81 SerGluAspGluAlaAspTyTyTyCyAlaAlaATrpaSpsAspSerLeuSerGlyTyrVal 100
Db      673 TCCGAGGATGAGGCTGATTTATTACTGTGCCTGCGACATCACCTCTCGGCTGGGTG 732
Qy      101 PheGlyGlyGlyThTyrsLeuThrValLeuGly 111
Db      733 TTCGGCGAGGAGCAACGCTGACCGTCTAGGT 765

RESULT 4
AAD32666
ID      AAD32666 standard; DNA; 846 BP.
XX      AC AAD32666;
XX      DT 29-AUG-2003 (revised)
XX      DT 18-JUN-2002 (first entry)
XX      DE Chimeric SCBP C6ML-3-9sfv'-L1-KDEL DNA.
XX      DE Chimeric SCBP C6ML-3-9sfv'-L1-KDEL DNA.
XX      KM Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
XX      KM nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
XX      KW gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX      OS Homo sapiens.
XX      OS Mus sp.
XX      OS Chimeric.
XX      PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
XX      DR WPI; 2002-268789/31.
XX      PT Gene-delivery compound for targeted gene delivery, comprises single-chain
XX      PT binding polypeptide having effector segment with cysteinyl residue and
XX      PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
XX      PT residue.

```

PN WO200200914-A2.
 XX 03-JAN-2002.
 XX 25-JUN-2001; 2001WO-US020182.
 XX 23-JUN-2000; 2000US-0213653P.
 XX (HUST/) HUSTON J S.
 PA (WILS/) WILS P.
 PA (QUAN/) QUAN Z.
 PA (LAUR/) LAURENT O.
 PA (MARA/) MARASCO W A.
 PA (SCHE/) SCHERMAN D.
 XX
 PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
 DR WPI; 2002-268789/31.
 DR P-PSDB; AAE20409.
 XX
 PT Gene-delivery compound for targeted gene delivery, comprises single-chain
 PT binding polypeptide having effector segment with cysteinyl residue and
 PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
 PT residue.
 XX
 XX Example 2; Fig 8; 96pp; English.
 XX
 CC The invention relates to gene-delivery compound comprising a single-chain
 CC binding polypeptide (SCBP) having at least one effector segment having a
 CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
 CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
 CC compound is useful for targeted gene delivery for treating diseases by
 CC gene therapy. The present sequence is chimeric SCBP C6ML-3-9SFV'-L2-KDEL
 CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 CC
 SQ Sequence 846 BP; 171 A; 250 C; 246 G; 179 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,45e-45 Length: 846
 Score: 566.00 Matches: 107
 Percent Similarity: 98.2% Conservative: 2
 Best Local Similarity: 96.4% Mismatches: 2
 Query Match: 96.3% Indels: 0
 DB: 6 Gaps: 0

US-10-092-640-36 (1-111) x AAD32666 (1-846)

QY 1 GlnSerValIeuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIle 20
 DB 433 CAGTCTGTGTTGACGCGAGCCGCCCTCAGTGTCTGCGGCCCCAGAGACAGAGGTCAACATC 492
 QY 21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTrpValSerTrpTyrGlnGlnIeu 40
 DB 493 TCCTGCTCTGGAAGCAGCTCCAAACATGGGAATTAATTATGATCCGGAACAGCAGCTC 552
 QY 41 ProGlyThAlaProIysIeuIeuIleTyrGlyHisThrAsnArgProIaGlyValPro 60
 DB 553 CAGAGAACGCCCCCAACTCCTCATCTATGATTCACACCAATGGGCCCAAGGGGCTCT 612
 QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 DB 613 GACCGATTCTCGGCTCCAGTCCAGTCTGSCACTCAGCTCTCCCTGCCATCACTGAGTTCCGG 672
 QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTAPAspSerIeuSerGlyTyrVal 100
 DB 673 TCCGAGGATGAGGCTGATTAATTACTGTGCTCTCGGACTACACCTCTCGGGCTGGGTG 732
 QY 101 PheGlyGlyGlyThrIysIeuThrValLeuGly 111
 DB 733 TTCCGGGAGAGAACCAAGCTGACCGTCTAAGT 765

RESULT 5

AAD32667
 ID AAD32667 standard; DNA; 861 BP.
 XX
 AC AAD32667;
 XX
 DT 29-AUG-2003 (revised)
 DT 18-JUN-2002 (first entry)
 XX
 DE Chimeric SCBP C6ML-3-9SFV'-L2-KDEL DNA.
 XX
 KW Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
 KW nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
 KW gene therapy; targeted gene delivery; human; murine; chimeric; ds.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..861
 FT /*tag= a
 FT /product= "Chimeric SCBP C6ML-3-9SFV'-L2-KDEL protein"
 FT /note= "CDS does not include start and stop codon"
 FT /partial

PN WO200200914-A2.
 XX 03-JAN-2002.
 XX 25-JUN-2001; 2001WO-US020182.
 XX 23-JUN-2000; 2000US-0213653P.
 XX (HUST/) HUSTON J S.
 PA (WILS/) WILS P.
 PA (QUAN/) QUAN Z.
 PA (LAUR/) LAURENT O.
 PA (MARA/) MARASCO W A.
 PA (SCHE/) SCHERMAN D.
 XX
 PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
 DR WPI; 2002-268789/31.
 DR P-PSDB; AAE20410.
 XX
 PT Gene-delivery compound for targeted gene delivery, comprises single-chain
 PT binding polypeptide having effector segment with cysteinyl residue and
 PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
 PT residue.
 XX
 XX Example 2; Fig 10; 96pp; English.

XX The invention relates to gene-delivery compound comprising a single-chain
 CC binding polypeptide (SCBP) having at least one effector segment having a
 CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
 CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
 CC compound is useful for targeted gene delivery for treating diseases by
 CC gene therapy. The present sequence is chimeric SCBP C6ML-3-9SFV'-L2-KDEL
 CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 CC
 SQ Sequence 861 BP; 173 A; 255 C; 250 G; 183 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,58e-45 Length: 861
 Score: 566.00 Matches: 107
 Percent Similarity: 98.2% Conservative: 2
 Best Local Similarity: 96.4% Mismatches: 2
 Query Match: 96.3% Indels: 0
 DB: 6 Gaps: 0

US-10-092-640-36 (1-111) x AAD32667 (1-861)

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Qy 1 GlnSerValIeuThrGlnProProSerValSerAlaIaIaProGlyGlnIlyValThrIle 20
Db 433 CAGTCTGTGTGACGACGCCCTCAGTGTCTGGGCCCCAGGACAGAAAGTACCATC 492
Qy 21 SerCySerGlySerSerSerAsnIleGlyAsnAsnTyValSerTPYrGlnGlnIleu 40
Db 493 TCCGCTCTCGAAGACACTCCAACTGGGAATATATGATTCCTGTCGACACACTC 552
Qy 41 ProGlyThraIaProIySleuIleuIleTyGlyVhiThraAsnArgProAlaGlyValPro 60
Db 553 CCGAGAACACGCCCAACTCCATCATCATGATCACCACCAATCGGCCGACGGGGTCCCT 612
Qy 61 AspArgPheSerGlySerIySerGlyThraSerAlaSerIleuAlaIleSerGlyPheArg 80
Db 613 GACCGATTCTCTGCTCAGTCTCAGTCTGSCACCTCCGCTCCGTCATCAGTGGGTTCGG 672
Qy 81 SerGluAspGluIaIaAspTYrTYrCyAlaAlaIaIaIaPheAspSerIleuSerGlyTPYrVal 100
Db 673 TCCGAGGATGAGGTGATTTATTACTGTGCTCCGAGACTACACCTCTCGGGCTGGGTG 732
Qy 101 PheGlyGlyGlyThryIySleuThrValIleuGly 111
Db 733 TTCGGCGAGAGAACCAAGCTGACCGTCTTAGT 765

RESULT 6
AAD32669
ID AAD32669 standard; DNA; 873 BP.
XX
AC AAD32669;
XX
DT 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
DE Chimeric SCBP C6ML-3-9sFv'-I2-nls DNA.
XX
KM Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
KM nucleic acid-binding moiety; NAM; lipid-associating moiety; LAM;
KM gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT 1..873
FT /*tag= a
FT /product= "Chimeric SCBP C6ML-3-9sFv'-I2-nls protein"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
PN WO200200914-A2.
XX
PD 03-JAN-2002.
XX
PF 25-JUN-2001; 2001WO-US020182.
XX
PR 23-JUN-2000; 2000US-0213653P.
XX
PA (HUST/) HUSTON J S.
PA (WILS/) WILS P.
PA (QUAN/) QUAN Z.
PA (LAUR/) LAURENT O.
PA (MARA/) MARASCO W A.
PA (SCHE/) SCHERMAN D.
XX
PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
XX
DR MPI; 2002-268789/31.
XX
DR P-PSDB; AAE20412.
XX
PT Gene-delivery compound for targeted gene delivery, comprises single-chain
PT binding polypeptide having effector segment with cysteinyl residue and
PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by

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PT residue.
XX
XX Example 2; Fig 14; 96pp; English.
PS
XX
CC The invention relates to gene-delivery compound comprising a single-chain
CC binding polypeptide (SCBP) having at least one effector segment having a
CC cysteinyl residue, and a nucleic acid-binding moiety (NAM) or a lipid-
CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
CC compound is useful for targeted gene delivery for treating diseases by
CC gene therapy. The present sequence is chimeric SCBP C6ML-3-9sFv'-I2-nls
CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 873 BP; 177 A; 260 C; 252 G; 184 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,69e-45 Length: 873
Score: 566.00 Matches: 107
Percent Similarity: 98.2% Conservative: 2
Best Local Similarity: 96.4% Mismatches: 2
Query Match: 96.3% Indels: 0
DB: Gaps: 0

US-10-092-640-36 (1-111) x AAD32669 (1-873)

Qy 1 GlnSerValIeuThrGlnProProSerValSerAlaIaIaProGlyGlnIlyValThrIle 20
Db 433 CAGTCTGTGTGACGACGCCCTCAGTGTCTGGGCCCCAGGACAGAAAGTACCATC 492
Qy 21 SerCySerGlySerSerSerAsnIleGlyAsnAsnTyValSerTPYrGlnGlnIleu 40
Db 493 TCCGCTCTCGAAGACACTCCAACTGGGAATATATGATTCCTGTCGACACACTC 552
Qy 41 ProGlyThraIaProIySleuIleuIleTyGlyVhiThraAsnArgProAlaGlyValPro 60
Db 553 CCGAGAACACGCCCAACTCCATCATCATGATCACCACCAATCGGCCGACGGGGTCCCT 612
Qy 61 AspArgPheSerGlySerIySerGlyThraSerAlaSerIleuAlaIleSerGlyPheArg 80
Db 613 GACCGATTCTCTGCTCAGTCTCAGTCTGSCACCTCCGCTCCGTCATCAGTGGGTTCGG 672
Qy 81 SerGluAspGluIaIaAspTYrTYrCyAlaAlaIaIaIaPheAspSerIleuSerGlyTPYrVal 100
Db 673 TCCGAGGATGAGGTGATTTATTACTGTGCTCCGAGACTACACCTCTCGGGCTGGGTG 732
Qy 101 PheGlyGlyGlyThryIySleuThrValIleuGly 111
Db 733 TTCGGCGAGAGAACCAAGCTGACCGTCTTAGT 765

RESULT 7
AAD32668
ID AAD32668 standard; DNA; 888 BP.
XX
AC AAD32668;
XX
DT 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
DE Chimeric SCBP C6ML-3-9sFv'-I2-H14 DNA.
XX
KM Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
KM nucleic acid-binding moiety; NAM; lipid-associating moiety; LAM;
KM gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT 1..888
FT /*tag= a
FT /product= "Chimeric SCBP C6ML-3-9sFv'-I2-H14 protein"
FT /note= "CDS does not include start and stop codon"
FT

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QY 21 SerCysSerGlySerSerSerSerAenllleGlyAsnAsnTrpValSerTrpYrGlnGlnLeu 40
 Db 61 TCTGTCTCTGGAGAGAGAGCTCCACATTGGAGATTAATTATCTCTGGTATCCAGCAGCTC 120
 QY 41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
 Db 121 CCAGGAACGGCCCCCAACTCCTCATCTATGTAACGCAATCGCCCTCAGGGGTCCT 180
 QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 Db 181 GACCGATTCTCTGGCTCCAGTCTGGCAGCTCCCTCGGCATCAGTGGGCTCCGG 240
 QY 81 SerGluAspGluAlaAspTrpTyrCysAlaAlaTrpAspSerLeuSerGlyTrpVal 100
 Db 241 TCCGAGATGAGGCTGATTATTAATCTGTGACAGATGGGATGACAGTGTGGTGGTG 300
 QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
 Db 301 TTGGCGGAGGAACCAAGCTGACGGTCTTAGGT 333
 RESULT 9
 ADN00519
 ID ADN00519 standard; DNA; 333 BP.
 AC ADN00519;
 DT 01-JUL-2004 (first entry)
 XX Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:6.
 DE human antibody; antibody; apolipoprotein B; atherosclerosis;
 KW passive immunisation; antiarteriosclerotic;
 KM anti-apolipoprotein B antibody; variable light region; VL; gene; ds.
 XX Homo sapiens.
 OS Synthetic.
 XX MO2004030698-A1.
 PN 15-APR-2004.
 PD 22-SEP-2003; 2003WO-SE001469.
 PF 04-OCT-2002; 2002SE-00002959.
 PR 27-AUG-2003; 2003SE-00002312.
 XX (FORS-) FORSKARPATENT I SYD AB.
 PA Nilsson J, Carlsson R, Bengtsson J, Strandberg L;
 PI WPI; 2004-316343/29.
 DR Use of a recombinant human antibody or antibody fragment directed towards
 PT at least one oxidized fragment of apolipoprotein B for the manufacture of
 PT a pharmaceutical composition for treating atherosclerosis.
 XX Claim 7; SEQ ID NO 6; 59pp; English.
 PS The present invention describes the use of at least one recombinant human
 CC antibody or antibody fragment directed towards at least one oxidised
 CC fragment of apolipoprotein B in the manufacture of a pharmaceutical
 CC composition for treatment of atherosclerosis by means of passive
 CC immunisation. Also described: (1) preparing the isolated antibody; (2)
 CC amplification of isolated human antibody; (3) passive immunisation of
 CC mammals; and (4) a pharmaceutical composition comprising the recombinant
 CC human antibody directed towards at least one oxidised fragment of
 CC apolipoprotein B for treatment of atherosclerosis by means of passive
 CC immunisation. The human antibody has antiarteriosclerotic activity. The
 CC isolated human antibody or antibody fragment directed towards at least
 CC one oxidised fragment of apolipoprotein B is useful in the manufacture of
 CC a pharmaceutical composition for treatment of atherosclerosis by means of
 CC passive immunisation. The present sequence represents a human anti-

CC apolipoprotein B antibody variable light region (VL) from the present
 CC invention.
 CC XX Sequence 333 BP; 66 A; 99 C; 93 G; 75 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 2.27e-43 Length: 333
 Score: 545.00 Matches: 102
 Percent Similarity: 95.5% Conservative: 4
 Best Local Similarity: 91.9% Mismatches: 5
 Query Match: 92.7% Indels: 0
 DB: 12 Gaps: 0
 US-10-092-640-36 (1-111) x ADN00519 (1-333)
 QY 1 GlnSerValLeuThrGlnProSerValSerAlaAlaProGlyGlnLysValThrIle 20
 Db 1 CACTGTGTGTGACTGACGACCACTCAGCCTCGGACCCCGGAGAGGTCACCATC 60
 QY 21 SerCysSerGlySerSerSerAenllleGlyAsnAsnTrpValSerTrpYrGlnGlnLeu 40
 Db 61 TCTTGTCTGGAAGCAGCTCCAAATATCGGAATTAATTATCTCTGGTATCCAGCAGCTC 120
 QY 41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
 Db 121 CCAGGAACGGCCCCCAACTCCTCATCTATGTAACGCAATCGCCCTCAGGGGTCCT 180
 QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 Db 181 GACCGATTCTCTGGCTCCAGTCTGGCAGCTCCCTCGGCATCAGTGGGCTCCGG 240
 QY 81 SerGluAspGluAlaAspTrpTyrCysAlaAlaTrpAspSerLeuSerGlyTrpVal 100
 Db 241 TCCGAGATGAGGCTGATTATTAATCTGTGACAGATGGGATGACAGTGTGGTGGTG 300
 QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
 Db 301 TTGGCGGAGGAACCAAGCTGACGGTCTTAGGT 333
 RESULT 10
 ADM98139
 ID ADM98139 standard; DNA; 333 BP.
 AC ADM98139;
 DT 01-JUL-2004 (first entry)
 XX Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:6.
 DE human antibody; antibody; apolipoprotein B; atherosclerosis;
 KW passive immunisation; antiarteriosclerotic; variable light region; VL;
 KM anti-apolipoprotein B antibody; gene; ds.
 XX Homo sapiens.
 OS Synthetic.
 XX MO2004030607-A2.
 PN 15-APR-2004.
 PD 06-OCT-2003; 2003WO-SE001547.
 PF 04-OCT-2002; 2002SE-00002959.
 PR 27-AUG-2003; 2003SE-00002312.
 PR 22-SEP-2003; 2003WO-SE001469.
 XX (FORS-) FORSKARPATENT I SYD AB.
 PA Nilsson J, Carlsson R, Bengtsson J, Strandberg L;
 PI WPI; 2004-316320/29.
 DR Use of an isolated human antibody or antibody fragment directed towards
 PT

PT at least one oxidized fragment of apolipoprotein B in the manufacture of
PT a pharmaceutical composition for treating atherosclerosis.
PS Claim 6; SEQ ID NO 6; 84pp; English.
XX
XX
XX The present invention describes the use of at least one isolated human
CC antibody or antibody fragment directed towards at least one oxidised
CC fragment of apolipoprotein B in the manufacture of a pharmaceutical
CC composition for treatment of atherosclerosis by means of passive
CC immunisation. Also described: (1) preparing the isolated antibody; (2)
CC amplifying the isolated human antibody; (3) passive immunisation of
CC mammals; and (4) a pharmaceutical composition comprising the isolated
CC human antibody directed towards at least one oxidised fragment of
CC apolipoprotein B for treatment of atherosclerosis by means of passive
CC immunisation, where the antibody is present in combination with a
CC pharmaceutical excipient. The human antibody has antiarteriosclerotic
CC activity. The isolated human antibody or antibody fragment directed
CC towards at least one oxidised fragment of apolipoprotein B is useful in
CC the manufacture of a pharmaceutical composition for treatment of
CC atherosclerosis by means of passive immunisation. The present sequence
CC represents a variable light region (VL) of an anti-apolipoprotein B
CC antibody from the present invention.
XX
SQ Sequence 333 BP; 66 A; 99 C; 93 G; 75 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,27e-43 Length: 333
Score: 545.00 Matches: 102
Percent Similarity: 95.5% Conservative: 4
Best Local Similarity: 91.9% Mismatches: 5
Query Match: 92.7% Indels: 0
DB: 12 Gaps: 0
US-10-092-640-36 (1-111) x ADM98139 (1-333)
QY 1 GlnSerValIleuThGlnProProSerValSerAlaAlaProGlyGlnIleValThrIle 20
DB 1 CAGTCTGTGCTGACTCAGCCACCTCAGGCTCGGAGCCCGGGAGAGGTCACCATC 60
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 61 TCTTGTCTGGAAGCGCTCCCAATATCGAAGATTAATGATCCGATACGACGCTC 120
QY 41 ProGlyThrAlaProIleuLeuLeuIleTyGlyHisThrAspArgProAlaGlyValPro 60
DB 121 CAGGAGAGCGCCCAAACTCTCATCTATGTAATCACTACATCGGCCCTCAGGGCTCCT 180
QY 61 AspArgPheSerGlySerIleSerSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
DB 181 GACCGATTCTCTGGCTCCAAAGTCTGGACCTCAGCTCCCTGGCCATCAGTGGCTCCGG 240
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTAspAspSerIleuSerGlyTyrVal 100
DB 241 TCCGAGGATGAGGCTGATTAATCTGTGACGATGGAGATGACGCTGAGTGGTGGTGG 300
QY 101 PheGlyGlyGlyThrIleuLeuThrValLeuGly 111
DB 301 TTGGCGGAGAGAACCAAGCTGACGATCTTAGGT 333
RESULT 11
ADM98163
ID ADM98163 standard; DNA; 333 BP.
XX
XX ADM98163;
XX 01-JUL-2004 (first entry)-
DE Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:30.
XX
XX human antibody; antibody; apolipoprotein B; atherosclerosis;
KW passive immunisation; antiarteriosclerotic; variable light region; VL;
KW anti-apolipoprotein B antibody; gene; ds.
XX

OS Homo sapiens.
OS Synthetic.
XX
XX WO2004030607-A2.
XX
XX 15-APR-2004.
XX
XX 06-OCT-2003; 2003WO-SE001547.
XX
XX 04-OCT-2002; 2002SE-00002959.
XX 27-AUG-2003; 2003SE-00002312.
XX 22-SEP-2003; 2003WO-SE001469.
XX
XX (FORS-) FORSKARPATENT I SYD AB.
XX
XX Nilsson J, Carlsson R, Bengtsson J, Strandberg L;
PI WPI; 2004-316320/29.
DR
XX
XX Use of an isolated human antibody or antibody fragment directed towards
PT at least one oxidized fragment of apolipoprotein B in the manufacture of
PT a pharmaceutical composition for treating atherosclerosis.
XX
XX
XX Claim 6; SEQ ID NO 30; 84pp; English.
XX
XX
XX The present invention describes the use of at least one isolated human
CC antibody or antibody fragment directed towards at least one oxidised
CC fragment of apolipoprotein B in the manufacture of a pharmaceutical
CC composition for treatment of atherosclerosis by means of passive
CC immunisation. Also described: (1) preparing the isolated antibody; (2)
CC amplifying the isolated human antibody; (3) passive immunisation of
CC mammals; and (4) a pharmaceutical composition comprising the isolated
CC human antibody directed towards at least one oxidised fragment of
CC apolipoprotein B for treatment of atherosclerosis by means of passive
CC immunisation, where the antibody is present in combination with a
CC pharmaceutical excipient. The human antibody has antiarteriosclerotic
CC activity. The isolated human antibody or antibody fragment directed
CC towards at least one oxidised fragment of apolipoprotein B is useful in
CC the manufacture of a pharmaceutical composition for treatment of
CC atherosclerosis by means of passive immunisation. The present sequence
CC represents a variable light region (VL) of an anti-apolipoprotein B
CC antibody from the present invention.
XX
SQ Sequence 333 BP; 65 A; 104 C; 93 G; 71 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.65e-42 Length: 333
Score: 536.00 Matches: 100
Percent Similarity: 94.6% Conservative: 5
Best Local Similarity: 90.1% Mismatches: 6
Query Match: 91.2% Indels: 0
DB: 12 Gaps: 0
US-10-092-640-36 (1-111) x ADM98163 (1-333)
QY 1 GlnSerValIleuThGlnProProSerValSerAlaAlaProGlyGlnIleValThrIle 20
DB 1 CAGTCTGTGCTGACTCAGCCACCTCAGGCTCGGAGCCCGGGAGAGGTCACCATC 60
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 61 TCTGCTCTGGAAGACCTCCCAATGTAATGTAATCTGATATCAGCAGCTC 120
QY 41 ProGlyThrAlaProIleuLeuLeuIleTyGlyHisThrAspArgProAlaGlyValPro 60
DB 121 CAGGAGAGCGCCCAAACTCTCATCTATGTAATCACTACATCGGCCCTCAGGGCTCCT 180
QY 61 AspArgPheSerGlySerIleSerSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
DB 181 GACCGATTCTCTGGCTCCAAAGTCTGGACCTCAGCTCCCTGGCCATCAGTGGCTCCGG 240
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTAspAspSerIleuSerGlyTyrVal 100

Db 241 TCCGAGGATGAGGCTGATTATTACTGTCGACGATGGGATGCCAGCTCACTGAGTGGGTG 300

Qy 101 PHEGLYGLYGLYThrLysLeuThrValLeuGly 111

Db 301 TTCGGCGAGAGAACCAAGCTGACGCTCTAGGT 333

RESULT 12

ID ADN00515 standard; DNA; 336 BP.

AC ADN00515;

DT 01-JUL-2004 (first entry)

DE Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:2.

KM human antibody; antibody; apolipoprotein B; atherosclerosis;

KM passive immunisation; antiarteriosclerotic;

OS Homo sapiens.

OS Synthetic.

PN WO2004030698-A1.

PD 15-APR-2004.

PF 22-SEP-2003; 2003WO-SE001469.

PR 04-OCT-2002; 2002SE-00002959.

PR 27-AUG-2003; 2003SE-00002312.

PA (FORS-) FORSKARPATENT I SYD AB.

PI Nilsson J, Carlsson R, Bengtsson J, Strandberg L;

DR WPI; 2004-316343/29.

PT Use of a recombinant human antibody or antibody fragment directed towards at least one oxidized fragment of apolipoprotein B for the manufacture of a pharmaceutical composition for treating atherosclerosis.

PS Claim 5; SEQ ID NO 2; 59pp; English.

XX The present invention describes the use of at least one recombinant human antibody or antibody fragment directed towards at least one oxidised

CC fragment of apolipoprotein B in the manufacture of a pharmaceutical

CC composition for treatment of atherosclerosis by means of passive

CC immunisation. Also described: (1) preparing the isolated antibody; (2)

CC amplification of isolated human antibody; (3) passive immunisation of

CC mammals; and (4) a pharmaceutical composition comprising the recombinant

CC human antibody directed towards at least one oxidised fragment of

CC apolipoprotein B for treatment of atherosclerosis by means of passive

CC immunisation. The human antibody has antiarteriosclerotic activity. The

CC isolated human antibody or antibody fragment directed towards at least

CC one oxidised fragment of apolipoprotein B is useful in the manufacture of

CC a pharmaceutical composition for treatment of atherosclerosis by means of

CC passive immunisation. The present sequence represents a human anti-

CC apolipoprotein B antibody variable light region (VL) from the present

CC invention.

XX SQ Sequence 336 BP; 69 A; 101 C; 93 G; 73 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2, 89e-42

Score: 533.50

Percent Similarity: 93.8%

Best Local Similarity: 90.2%

Query Match: 90.7%

DB: 12

Length: 336

Matches: 101

Conservative: 4

Mismatches: 6

Indels: 1

Gaps: 1

US-10-092-640-36 (1-111) x ADN00515 (1-336)

Qy 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20

Db 1 CAGCTGTGTGCTGCTAGCCACCTCTAGCCTCTGGAGACCCCGGACAGAGGTCACCATC 60

Qy 21 SerCySerSerGlySerSerSerSerAniIleGlyAsnAsnTyrValSerTyrTyrGlnGlnLeu 40

Db 61 TCCGTGCTCGAAGACAGGTCCACATCTGGGAATTAATTATGTAATCCGTATGACGAGCTC 120

Qy 41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60

Db 121 CCAGAAACGGCCCCCAACTCCATCTAGTATGTAACAACATGCGCCCTCAGGCGCTCCCT 180

Qy 61 AspArgPheSerGlySerGlySerGlyTyrThrSerAlaSerLeuAlaIleSerGlyPheArg 80

Db 181 GACCGATTCCTGCTGCTCAAGCTGCGACCTCAGCCTCCCTGGCAACAGTGGCTCCG 240

Qy 81 SerGluAspGlyValAspTyrTyrCysAlaAlaTyrAspAspSerLeuSerGly---Tyr 99

Db 241 TCCGAGGATGAGGCTGATTATTACTGTCGACGATGGGATGACAGCTGAATGTCATTGG 300

Qy 100 ValPheGlyGlyGlyThrLysLeuThrValLeuGly 111

Db 301 GTGTTGCGGAGAGAACCAAGCTGACGCTCTAGGT 336

RESULT 13

ID ADM98135 standard; DNA; 336 BP.

AC ADM98135;

DT 01-JUL-2004 (first entry)

DE Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:2.

KM human antibody; antibody; apolipoprotein B; atherosclerosis;

KM passive immunisation; antiarteriosclerotic; variable light region; VL;

OS Homo sapiens.

OS Synthetic.

PN WO2004030607-A2.

PD 15-APR-2004.

PF 06-OCT-2003; 2003WO-SE001547.

PR 04-OCT-2002; 2002SE-00002959.

PR 27-AUG-2003; 2003SE-00002312.

PR 22-SEP-2003; 2003WO-SE001469.

PA (FORS-) FORSKARPATENT I SYD AB.

PI Nilsson J, Carlsson R, Bengtsson J, Strandberg L;

DR WPI; 2004-316320/29.

PT Use of an isolated human antibody or antibody fragment directed towards at least one oxidized fragment of apolipoprotein B in the manufacture of a pharmaceutical composition for treating atherosclerosis.

PS Claim 6; SEQ ID NO 2; 84pp; English.

XX The present invention describes the use of at least one isolated human antibody or antibody fragment directed towards at least one oxidised

CC fragment of apolipoprotein B in the manufacture of a pharmaceutical

CC composition for treatment of atherosclerosis by means of passive

CC immunisation. Also described: (1) preparing the isolated antibody; (2)

CC amplifying the isolated human antibody; (3) passive immunisation of

CC mammals; and (4) a pharmaceutical composition comprising the isolated

CC human antibody directed towards at least one oxidised fragment of

CC apolipoprotein B for treatment of atherosclerosis by means of passive

CC immunisation, where the antibody is present in combination with a

CC pharmaceutical excipient. The human antibody has antiarteriosclerotic
CC activity. The isolated human antibody or antibody fragment directed
CC towards at least one oxidised fragment of apolipoprotein B is useful in
CC the manufacture of a pharmaceutical composition for treatment of
CC atherosclerosis by means of passive immunisation. The present sequence
CC represents a variable light region (VL) of an anti-apolipoprotein B
CC antibody from the present invention.

XX SQ Sequence 336 BP; 69 A; 101 C; 93 G; 73 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,89e-42	Length:	336
Score:	533.50	Matches:	101
Percent Similarity:	93.8%	Conservative:	4
Best Local Similarity:	90.2%	Mismatches:	6
Query Match:	90.7%	Indels:	1
DB:	12	Gaps:	1

US-10-092-640-36 (1-111) x ADM98135 (1-336)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIle 20
DB 1 CAGTCTGTCGCTACCTCAGCCACCTCAGCGTGGAGACCCCGGCGAGGGGTCAACCATC 60
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 61 TCTCTGCTCGAAGCAGGTCCTCAACATCTGGGAATTAATGATCTCTGGATACAGCTTC 120
QY 41 ProGlyThrAlaProIleuLeuLeuIleTyrglyHisThrAsnArgProAlaGlyValPro 60
DB 121 CAGGAAACGGCCCCCAACTCTCATCTATGTGTAACAAACATCGGCTTCAGGGGTCCCT 180
QY 61 AspArgPheSerGlySerIleSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 181 GACCATTCCTCGGCTCCCAAGTCGCGACCTCAGCTCCCTGCGCATCGTGGCTCCGG 240
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTatPaspAspSerLeuSerGly--Tyr 99
DB 241 TCCGAGGAGAGGCGCTGATTAATCTGTGACGATGGAGACAGCTGTAATGCTCATTTGG 300

QY 100 ValPheGlyGlyGlyThrIleLeuThrValLeuGly 111
DB 301 GTGTTGCGGCGAGAAACCAAGCTGACGCTCTAGGT 336

RESULT 14

ID ADM98167 standard; DNA; 333 BP.

XX ADM98167;

DT 01-JUL-2004 (first entry)

XX Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:34.

XX human antibody; antibody; apolipoprotein B; atherosclerosis;

XX passive immunisation; antiarteriosclerotic; variable light region; VL;

XX anti-apolipoprotein B antibody; gene; ds.

OS Homo sapiens.

OS Synthetic.

PN WO2004030607-A2.

PD 15-APR-2004.

PF 06-OCT-2003; 2003WO-SE001547.

PR 04-OCT-2002; 2002SE-00002959.

PR 27-AUG-2003; 2003SE-00002312.

PR 22-SEP-2003; 2003WO-SE001465.

XX (FORS-) FORSKARPATENT I SYD AB.

PI Nilsson J, Carlsson R, Bengtsson J, Strandberg L;
XX WPI, 2004-316320/29.

XX Use of an isolated human antibody or antibody fragment directed towards
XX at least one oxidized fragment of apolipoprotein B in the manufacture of
XX a pharmaceutical composition for treating atherosclerosis.

PS Claim 6; SEQ ID NO 34; 84pp; English.

XX The present invention describes the use of at least one isolated human
XX antibody or antibody fragment directed towards at least one oxidised
XX fragment of apolipoprotein B in the manufacture of a pharmaceutical
XX composition for treatment of atherosclerosis by means of passive
XX immunisation. Also described: (1) preparing the isolated antibody; (2)
XX amplifying the isolated human antibody; (3) passive immunisation of
XX mammals; and (4) a pharmaceutical composition comprising the isolated
XX human antibody directed towards at least one oxidised fragment of
XX apolipoprotein B for treatment of atherosclerosis by means of passive
XX immunisation, where the antibody is present in combination with a
XX pharmaceutical excipient. The human antibody has antiarteriosclerotic
XX activity. The isolated human antibody or antibody fragment directed
XX towards at least one oxidised fragment of apolipoprotein B is useful in
XX the manufacture of a pharmaceutical composition for treatment of
XX atherosclerosis by means of passive immunisation. The present sequence
XX represents a variable light region (VL) of an anti-apolipoprotein B
XX antibody from the present invention.

SQ Sequence 333 BP; 68 A; 102 C; 92 G; 71 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	4,96e-42	Length:	333
Score:	531.00	Matches:	99
Percent Similarity:	93.7%	Conservative:	5
Best Local Similarity:	89.2%	Mismatches:	7
Query Match:	90.3%	Indels:	0
DB:	12	Gaps:	0

US-10-092-640-36 (1-111) x ADM98167 (1-333)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIle 20

DB 1 CAGTCTGTCGCTACCTCAGCCACCTCAGCGTCTGGAGACCCCGGCGAGGGGTCAACCATC 60

QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40

DB 61 TCTCTGCTCGAAGCAGGTCCTCAACATCTGGGAATTAATGATCTCTGGATACAGCTTC 120

QY 41 ProGlyThrAlaProIleuLeuLeuIleTyrglyHisThrAsnArgProAlaGlyValPro 60

DB 121 CAGGAAACGGCCCCCAACTCTCATCTATGTGTAACAAACATCGGCTTCAGGGGTCCCT 180

QY 61 AspArgPheSerGlySerIleSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80

DB 181 GACCATTCCTCGGCTCCCAAGTCGCGACCTCAGCTCCCTGCGCATCGTGGCTCCGG 240

QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTatPaspAspSerLeuSerGlyTyrVal 100

DB 241 TCCGAGGAGAGGCGCTGATTAATCTGTGACGATGGAGACAGCTCGTGGCTG 300

QY 101 PheGlyGlyGlyThrIleLeuThrValLeuGly 111

DB 301 TTGCGCGAGAGAACCAAGCTGACGCTCTAGGT 333

RESULT 15

ID ADN00521 standard; DNA; 333 BP.

XX ADN00521;

DT 01-JUL-2004 (first entry)

DE Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:8.

XX human antibody; antibody; apolipoprotein B; atherosclerosis;
 KW passive immunisation; antiarteriosclerotic;
 KW anti-apolipoprotein B antibody; variable light region; VL; gene; ds.
 OS Homo sapiens.
 OS Synthetic.
 XX MO2004030698-A1.
 PD 15-APR-2004.
 PF 22-SEP-2003; 2003MO-SE001469.
 XX 04-OCT-2002; 2002SE-00002859.
 PR 27-AUG-2003; 2003SE-00002312.
 XX (FORS-) FORSKARPATENT I SYD AB.
 PA Nilsson J, Carlsson R, Bengtsson J, Strandberg L;
 PI WPI, 2004-316343/29.
 DR
 XX
 XX
 PT Use of a recombinant human antibody or antibody fragment directed towards
 PT at least one oxidized fragment of apolipoprotein B for the manufacture of
 PT a pharmaceutical composition for treating atherosclerosis.
 XX
 PS Claim 8; SEQ ID NO 8; 59pp; English.
 XX
 XX The present invention describes the use of at least one recombinant human
 CC antibody or antibody fragment directed towards at least one oxidised
 CC fragment of apolipoprotein B in the manufacture of a pharmaceutical
 CC composition for treatment of atherosclerosis by means of passive
 CC immunisation. Also described: (1) preparing the isolated antibody; (2)
 CC amplification of isolated human antibody; (3) passive immunisation of
 CC mammals; and (4) a pharmaceutical composition comprising the recombinant
 CC human antibody directed towards at least one oxidised fragment of
 CC apolipoprotein B for treatment of atherosclerosis by means of passive
 CC immunisation. The human antibody has antiarteriosclerotic activity. The
 CC isolated human antibody or antibody fragment directed towards at least
 CC one oxidised fragment of apolipoprotein B is useful in the manufacture of
 CC a pharmaceutical composition for treatment of atherosclerosis by means of
 CC passive immunisation. The present sequence represents a human anti-
 CC apolipoprotein B antibody variable light region (VL) from the present
 CC invention.
 XX
 SQ Sequence 333 BP; 69 A; 103 C; 89 G; 72 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 7.71e-42 Length: 333
 Score: 529.00 Matches: 99
 Percent Similarity: 92.8% Conservative: 4
 Best Local Similarity: 89.2% Mismatches: 8
 Query Match: 90.0% Indels: 0
 DB: 12 Gaps: 0
 US-10-092-640-36 (1-111) x ADN00521 (1-333)
 QY 1 GlnSerValIleuThrgInProSerValSerAlaAlaProGlyGlnIuysValThrIle 20
 Db 1 CAGTGTGTCTGACTGACGACCACTCAGCGTCTGGAGACCCCGGCGAGAGGTCAACATC 60
 QY 21 SerCysSerGlySerSerSerAenIIleGlyAenAenTyValSerTrpTyrgInGlnIleu 40
 Db 61 TCTGCTCTGGAAGCAGCTCAACATGGAAATGATATGATATCTGATATCAGCAGCTC 120
 QY 41 ProGlyThrAlaProIysIleuIleuIleTyrgIyHisThrAsnAyrProIaGlyValPro 60
 Db 121 CCGGAAACGGCCCAACCTCCATCTATAGTAATATACGCGCCCTCAGGGGTCCTCCT 180
 QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
 Db 181 GACCGATTCTCTGGCTCCAAAGTGTGCACTCACTCCCTGCGCATCACTGAGGCTCCGG 240

QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaTrpAspAspSerIleuSerGlyTrpVal 100
 Db 241 TCCGAGGATGAGGCTGTATTAATCTGTGCAGCATGGATGACAGCTGAGTCAATTGGCTG 300
 QY 101 PheGlyGlyGlyThrIysLeuThrValIleuGly 111
 Db 301 TTGCGCGGAGGAAACCAAGCTGACGCTCTTAGGT 333

Search completed: May 25, 2006, 16:28:20
 Job time : 476.137 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:28:39 ; Search time 3650.05 Seconds

(without alignments)
2550.806 Million cell updates/sec

Title: US-10-092-640-36

Perfect score: 588

Sequence: 1 QSVLQNPSPVSAAPGQKVTI.....WDSLSGWVGGGKTULVUG 111

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
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2	527	89.6	902	3 BQ883560	BQ883560 AGENCOURT
3	519	88.3	490	5 CD692216	CD692216 EST8739 h
4	516.5	87.8	548	9 DA992977	DA992977 DA992977

SUMMARIES

5	516	87.8	494	4	BX283265	BX283265
6	516	87.8	512	2	BM314111	BM314111 h07c03.y
7	516	87.8	656	2	BG755949	BG755949 602716426
8	515.5	87.7	552	9	DA978161	DA978161
9	512	87.1	873	2	BG686011	BG686011 602638561
10	511	86.9	780	2	BG535669	BG535669 602563379
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12	509	86.6	578	9	DA920210	DA920210
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14	509	86.6	680	2	BG745508	BG745508 602724089
15	508	86.4	498	7	AM405612	AM405612 UI-HF-BLO
16	507	86.2	574	5	CD689899	CD689899 EST6422 h
17	507	86.2	985	2	BG758331	BG758331 602712522
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19	504.5	85.8	620	5	CD696969	CD696969 EST13492
20	503	85.5	561	7	AM406077	AM406077 UI-HF-BLO
21	502	85.4	1029	2	BG760087	BG760087 602733341
22	500	85.0	823	2	BG686957	BG686957 602650951
23	499	84.9	526	9	DA915919	DA915919
24	499	84.9	906	2	BP975920	BP975920 602246119
25	498	84.7	419	7	AM631244	AM631244 h173102.y
26	498	84.7	600	5	CD704266	CD704266 EST20793
27	497	84.5	470	5	CD698832	CD698832 EST15355
28	497	84.5	560	9	DA922062	DA922062 DA922062
29	497	84.5	783	2	BM007830	BM007830 603617507
30	497	84.5	817	2	BG542829	BG542829 602571593
31	496.5	84.4	387	2	BG979831	BG979831 CM4-CN009
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33	495.5	84.3	567	9	DA929121	DA929121 DA929121
34	494	84.0	730	5	CD709117	CD709117 EST25644
35	493.5	83.9	926	3	BQ706329	BQ706329 AGENCOURT
36	493	83.8	403	7	BE164159	BE164159 QV2-HT046
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39	493	83.8	894	3	BQ708570	BQ708570 AGENCOURT
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ALIGNMENTS

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DEFINITION	DA975812 SYN0V2 Homo sapiens cDNA clone SYN0V2006376 5', mRNA				
ACCESSION	DA975812	GI:82348404			
VERSION	DA975812.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 559)				
AUTHORS	Kimura,K., Makamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakagiri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,K., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuna,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanabe,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.				
TITLE	Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes				
JOURNAL	Genome Res. 16 (1), 55-65 (2006)				
PUBMED	16344560				
COMMENT	Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute				

REFERENCE
AUTHORS
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo
 1 (bases 1 to 490)
 Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
 Zeng, Y.-X.
TITLE
 Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL
 Unpublished (2003)
COMMENT
 Contact: Yixin Zeng
 Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@rsu.su.cn.
FEATURES
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 Percent Similarity: 91.9% Conservative: 4
 Best Local Similarity: 88.3% Mismatches: 9
 Query Match: 88.3% Indels: 0
 DB: 5 Gaps: 0

US-10-092-640-36 (1-111) x CD692216 (1-490)

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DB 117 CAGTCGTGTGCTGACTGACCACTCAGCTCTGGAGCCCGGCGAGAGGTCACCATC 176
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QY 21 SerCySerGlySerSerSerSerAenIleGlyAsnAsnTyTValSerTPYrGlnGlnLeu 40
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DB 177 TCTTGTCTTGGAGACGATTCGAATATGAAATATATATGTAATGTCGACCACTC 236
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QY 41 ProGlyThrAlaProlySleuLeuIleTyTgLyHisThrAsnArgProAlaGlyValPro 60
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DB 237 CCGAGAACGGCCCAAGCTCTCATCTATAGGAACAATCAGCAGCCCTAGGGGTCCT 296
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QY 61 AspArgPheSerGlySerTySerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
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QY 81 SerGluAspGluAlaAspTyTyrCyAlaAlaIleTTPAspAspSerLeuSerGlyTTPVal 100
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QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
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 version DA992977.1 GI:83070668
 keywords EST.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
REFERENCE
 1 (bases 1 to 548)

AUTHORS
 Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsutsumi, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T., and Sugano, S.
TITLE
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
JOURNAL
 PLoS ONE
PUBMED
 16344560
COMMENT
 Contact: Takao Isogai
 R1J Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: tji-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.
FEATURES
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 Query Match: 87.8% Indels: 1
 DB: 9 Gaps: 1

US-10-092-640-36 (1-111) x DA992977 (1-548)

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DB 104 CAGTCGTGTGCTGACTGACCACTCAGCTCTGGAGCCCGGCGAGAGGTCACCATC 163
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QY 21 SerCySerGlySerSerSerSerAenIleGlyAsnAsnTyTValSerTPYrGlnGlnLeu 40
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DB 164 TCTTGTCTTGGAGACGATTCGAATATGAAATATATGTAATGTCGACCACTC 223
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QY 41 ProGlyThrAlaProlySleuLeuIleTyTgLyHisThrAsnArgProAlaGlyValPro 60
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DB 224 CCGAGAACGGCCCAAGCTCTCATCTATAGGAACAATCAGCAGCCCTAGGGGTCCT 293
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QY 61 AspArgPheSerGlySerTySerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
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DB 284 GACCGATTCTCTGGCTCCAGCTGCAAGCTCAGCTCCCTGGCCATCAGTGCATCCGG 343
 |||||
QY 81 SerGluAspGluAlaAspTyTyrCyAlaAlaIleTTPAspAspSerLeuSerGlyTTPVal 99
 |||||
DB 344 TCCGAGAGATGAGGCTGATATTATGTCAGCATGGATGACAGCTGAGTGGTGGTC 403
 |||||
QY 100 ValPheGlyGlyGlyThrLysLeuThrValLeuGly 111
 |||||
DB 404 GTTTCGGCGAGGAGCAAGCTGACCGTCTTAGGT 439
 |||||

RESULT 5
 BX283265 494 bp mRNA linear EST 04-MAR-2003
 LOCUS BX283265

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DEFINITION BX283265 NIH_MGC_48 Homo sapiens cDNA clone IMAGE958D081707 ;
IMAGE:4856407, mRNA sequence.
ACCESSION BX283265
VERSION BX283265.1 GI:28847719
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 494)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, R., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE958D081707.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection:
http://www.rzpd.de/Clonedata/cgi-
bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heuberweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
PCMW-M31u, Primer sequence: CGTTGTAAACGACGCGCACT.
Location/Qualifiers
1..494
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE958D081707 ; IMAGE:4856407"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1.51e-45 Length: 494
Score: 516.00 Matches: 99
Percent Similarity: 91.2% Conservative: 4
Best Local Similarity: 87.6% Mismatches: 8
Query Match: 87.8% Indels: 2
DB: 4 Gaps: 1
US-10-092-640-36 (1-111) x BX283265 (1-494)

QY 1 GInSeValleuThrGInProSeRValSeRAlaAlaProGlyGInIysValThrIle 20
Db 90 CAGTGTGTCCTAGCTACGACCACTCAGCGCTCGGAGACCCCGGAGAGGCGTCACTAC 149
QY 21 SerCySeSeGlySeSeSeSerAenIllegIyAsnAsnIyValSeRTrpTyGInGInIeu 40
Db 150 TCTTGTTCTGGAAGCAGCTCCAAACATCGGAAGTAATTATGTAATCTGTACACGACGCTC 209
QY 41 ProGlyThAlaProIySeuIeuIeTyGlyHIthAsnArgProAlaGlyValPro 60
Db 210 CCAAGAAAGCGCCCAAACTCCTCATCTATAGGAATATATCAGCGCCCTCAGAGGCTCCT 269

```

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QY 61 AspArgPheSeSeGlySeRlySeSeRgLyThrSeRAlaSeRLeuAlaIleSeRgLyPheArg 80
Db 270 GACCCATTCTCTGGCTCCAGGCTGTGGCACCTCAGCGCTCCCTGGCCATCATGTGGCTCCGG 329
QY 81 SerGluAspGluAlaAspTyTyTyCyAlaAlaIatPAspAspSeRlySeSeGly----- 98
Db 330 TCCGAGGATGAGCGCTGATTATTACTGTGACGATGGATGACAGCTGAGTGTCCCAAT 389
QY 99 TrpValPheGlyGlyGlyThryIeuThrValIleuGly 111
Db 390 TGGGTGTTCCGGGAGGAGGACCAAGCTGACCGTCTTAGGT 428

RESULT 6
BM314111
LOCUS BM314111
DEFINITION 512 bp mRNA linear EST 03-JAN-2002
ih07c03.y1 Human insulinoma Homo sapiens cDNA 5' similar to
SW:LVIG HUMAN P06316 IG LAMBDA CHAIN V-I REGION BLZ PRECURSOR. ;
mRNA sequence.
BM314111
ACCESSION BM314111.1 GI:18048456
VERSION BM314111
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 512)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scaer, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarashvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
Location/Qualifiers
1..512
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN
Alignment Scores:
Pred. No.: 1.59e-45 Length: 512
Score: 516.00 Matches: 96

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Percent Similarity: 91.9% Conservative: 6
 Best Local Similarity: 86.5% Mismatches: 9
 Query Match: 87.8% Indels: 0
 DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x BM314111 (1-512)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlnGlnValThrIle 20
 |||
 DB 75 CAGTCTGTGCTGACTGACGACCCCTCAGCGCTCGGACCCCGGAGAGGTCACCATC 134
 QY 21 SerCysSerGlySerSerSerSerAenIleGlyAsnAsnTyValSerTPYrGlnGlnLeu 40
 |||
 DB 135 TCTGTGTTCTGAGAGAGCTCCACATCGCGGTAATCATGTAACTGTATCAGCAATC 194
 QY 41 ProGlyThrAlaProLyLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro 60
 |||
 DB 195 CCAAGAAACGGCCCCCAAAAGTCTCATCTATAGAAATAATCAGCGGCGCTCAGAGGTCCTC 254
 QY 61 AspArgPheSerGlySerSerSerSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 |||
 DB 255 GACCGATTCTCCGGCTCCAAAGTCTGACCTCAGCCCTCCGTCATCAGTGAATCGCG 314
 QY 81 SerGluAspGluAlaAspTYrTYrCYaAlaAlaTrpAspAspSerLeuSerGlyTPYrVal 100
 |||
 DB 315 TCCGAGATGATGAGCTGATTTACTGTGACGATGGATGACAGCTGATGTTGGGTG 374
 QY 101 PheGlyGlyGlyThrTyLeuThrValLeuGly 111
 |||
 DB 375 TTCGGCGAGAGGACCAAGTGCCTGCTAGGT 407

RESULT 7
 BG755949 656 bp mRNA linear EST 15-MAY-2001
 LOCUS 602716426F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856407 5',
 DEFINITION mrna sequence.

ACCESSION BG755949
 VERSION BG755949.1 GI:14066602
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 2 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 3 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 4 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 5 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 6 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 7 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 8 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 9 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 10 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 11 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE 12 (bases 1 to 656)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straube, Ph.D.
 Email: cgabbs-r@mail.nih.gov

ORIGIN

Alignment Scores:

Pred. No.: 2.18e-45 Length: 656
 Score: 516.00 Matches: 99
 Percent Similarity: 91.2% Conservative: 4
 Best Local Similarity: 87.6% Mismatches: 8
 Query Match: 87.8% Indels: 2
 DB: 2 Gaps: 1

US-10-092-640-36 (1-111) x BG755949 (1-656)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlnGlnValThrIle 20
 |||
 DB 90 CAGTCTGTGCTGACTGACGACCCCTCAGCGCTCGGACCCCGGAGAGGTCACCATC 149
 QY 21 SerCysSerGlySerSerSerSerAenIleGlyAsnAsnTyValSerTPYrGlnGlnLeu 40
 |||
 DB 150 TCTGTGTTCTGAGAGAGCTCCACATCGCGGTAATCATGTAACTGTATCAGCAATC 209
 QY 41 ProGlyThrAlaProLyLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro 60
 |||
 DB 210 CCAAGAAACGGCCCCCAAAAGTCTCATCTATAGAAATAATCAGCGGCGCTCAGAGGTCCTC 269
 QY 61 AspArgPheSerGlySerSerSerSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 |||
 DB 270 GACCGATTCTCCGGCTCCAAAGTCTGACCTCAGCCCTCCGTCATCAGTGAATCGCG 329
 QY 81 SerGluAspGluAlaAspTYrTYrCYaAlaAlaTrpAspAspSerLeuSerGlyTPYrVal 98
 |||
 DB 330 TCCGAGATGATGAGCTGATTTACTGTGACGATGGATGACAGCTGATGTTGGGTG 389
 QY 99 TrpValPheGlyGlyGlyThrTyLeuThrValLeuGly 111
 |||
 DB 390 TGGGTGTCGGCGAGGAGCAAGTGCCTGCTAGGT 428

RESULT 8

DA978161 552 bp mRNA linear EST 15-NOV-2005
 LOCUS DA978161 SYN0V2 Homo sapiens cDNA clone SYN0V2009255 5', mRNA
 DEFINITION sequence.

ACCESSION DA978161
 VERSION DA978161.1 GI:82436709
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 552)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, Y., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

REFERENCE 2 (bases 1 to 552)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, Y., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

REFERENCE 3 (bases 1 to 552)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, Y., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

REFERENCE 4 (bases 1 to 552)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, Y., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

REFERENCE 5 (bases 1 to 552)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, Y., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

REFERENCE 6 (bases 1 to 552)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, Y., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

REFERENCE 7 (bases 1 to 552)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, Y., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

REFERENCE 8 (bases 1 to 552)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, Y., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

REFERENCE 9 (bases 1 to 552)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, Y., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.

FEATURES
source
1. 552
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SYNOV2009255"
/tissue_type="synovial membrane tissue from rheumatoid
arthritis"
/clone_lib="SYNOV2"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.: 1,98e-45 Length: 552
Score: 515.50 Matches: 99
Percent Similarity: 91.1% Conservative: 9
Best Local Similarity: 88.4% Mismatches: 1
Query Match: 87.7% Indels: 1
DB: 9 Gaps: 1

US-10-092-640-36 (1-111) x DA978161 (1-552)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
DB 104 CAGTCTGTCTGCTACCTCAGCCACCCTCAGCGTCTGGAGCCCGGAGAGGGTCAACATC 163
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 164 TCTTGTCTCGAAGCAGCTCCACATCAGAAATTAATTATCTCTCTGTAACAGCAGCTC 223
QY 41 ProGlyThrAlaProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 224 CCAGGAGCGGGCCCCCAACTCCTCATCTATGAAATATCAGCGGCGCTCAGGGGCTCCT 283
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 284 GACCGATTCTCGGCTCCCAAGCTCGACCTCAGCTCCCTGGCCATCGTGGGCTCCGG 343
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTTPAspAspSerLeuSerGly--TTP 99
DB 344 TCCGAGGATGAGGCTCTTATTAATCTGCAACATGGAGATGACAGCTGAGTGTCTTGG 403
QY 100 ValPheGlyGlyGlyThrLysLeuThrValLeuGly 111
DB 404 GTGTCGGCGGAGGAGCAAGCTGACGCTGAGT 439

RESULT 9

RG686011 873 bp mRNA linear EST 01-MAY-2001
LOCUS BG686011
DEFINITION 602538561F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766295 5',
mRNA sequence.

ACCESSION BG686011
VERSION BG686011.1 GI:13917395
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 873)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1626 row: 1 column: 16
High quality sequence stop: 842.

FEATURES
source
1. 873
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4766295"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOT7; Site: 1: XhoI;
Site: 2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 8,54e-45 Length: 873
Score: 512.00 Matches: 95
Percent Similarity: 91.9% Conservative: 7
Best Local Similarity: 85.6% Mismatches: 9
Query Match: 87.1% Indels: 0
DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x BG686011 (1-873)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
DB 88 CAGTCTGTCTGCTACCTCAGCCACCCTCAGCGTCTGGAGCCCGGAGAGGGTCAACATC 147
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 148 TCTTGTCTCGAAGCAGCTCCCAACATCGAATTAATCTGTAACCTGTAACAGCAGCTC 207
QY 41 ProGlyThrAlaProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 208 CCAGGAGCGGGCCCCCAACTCCTCATCTATGAAATATCAGCGGCGCTCAGGGGCTCCT 267
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 268 GACCGATTCTCGGCTCCCAAGCTCGACCTCAGCTCCCTGGCCATCGTGGGCTCCAG 327
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTTPAspAspSerLeuSerGlyTTPVal 100
DB 328 TCTGAGGATGAGGCTGATTAATTAATCTGACAGATGGAGATGACAGCTGATGTTGGTG 387
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
DB 388 TTGCGGAGGAGGACCAAGCTGACGCTCTAGGT 420

RESULT 10

RG535669 780 bp mRNA linear EST 03-APR-2001
LOCUS BG535669
DEFINITION 602563379F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4688082 5',
mRNA sequence.

ACCESSION BG535669
VERSION BG535669.1 GI:13527214
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 780)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 plate: LNCM501 row: n column: 19
 high quality sequence stop: 707.
 Location/Qualifiers

FEATURES

source

```

1. 780
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:468082"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1b="NIH MGC 77"
/notes="Organism: lung; Vector: pDNR-LIB (Clontech); Site: 1;
5' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCATTTATGGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCCGAGCGCCGACATC-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."

```

ORIGIN

Alignment Scores:

Pred. No.: 9, 48e-45 Length: 780
 Score: 511.00 Matches: 96
 Percent Similarity: 91.0% Conservative: 5
 Best Local Similarity: 86.5% Mismatches: 10
 Query Match: 86.9% Indels: 0
 DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x BG535669 (1-780)

```

QY 1 GlnSerValleuthThgInpProSerValSerAlaAlaProGlyGlnValThrIle 20
DB 105 CAGTCTGTGCTGACTCAGCCACCTCAGCGTGGAGCCCGGAGAGGATCACCATC 164
QY 21 SerCysSerGlySerSerSerAniIleGlyAsnAsnTyValSerTrpTyrgInGlnIleu 40
DB 165 TCTTGTTCGGAAGCACTCCAACTCGGAAGTAACATGTATACCTGGTCCGCAATTC 224
QY 41 ProGlyThrAlaProlybLeuLeuIleTyrgLysIleThrAsnArgProAlaGlyValPro 60
DB 225 CCAAGAACCGCCCCCAAACTCTCATCTATAGAAATATAGAGGCGCTTAGGGATCCCT 264
QY 61 AspArgPheSerGlySerIlySerGlyThnSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 285 GACCGATCTCTGGCTCCAACTCTGACCTGACCTCCCTGACATCAGTGGGCTCCGG 344
QY 81 SerGluAspGluAlaAspTrpTyrgAlaAlaIleTrpAspAspSerLeuSerGlyTrpVal 100
DB 345 TCCGAGATGAGGCTATTAATTAATGAGCATGGAGATGACAGCTGAGTGGGTGGGTG 404
QY 101 PheGlyGlyGlyThrIlySerLeuThrValLeuGly 111
DB 405 TTCGGCGAGAGGACCAAGCTGACCTCTTAGGT 437

```

RESULT 11
 DA971136 566 bp mRNA linear EST 11-NOV-2005
 LOCUS DA971136
 DEFINITION DA971136 STNOV2 Homo sapiens cdna clone STNOV2000476 5', mRNA

ACCESSION DA971136
 VERSION DA971136.1
 KEYWORDS GI:82082025
 SOURCE EST.
 ORGANISM Homo sapiens (human)

REFERENCE

sequence.
 1 (bases 1 to 566)
 Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsutitani, K., Makaguti, H.,
 Iehi, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuchida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

TITLE

JOURNAL PUMED
 COMMENT

Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3966
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan): cDNA library construction:
 Helix Research Institute (HRI), 5' end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3' end one
 pass sequencing: RAB.
 Location/Qualifiers

FEATURES

source

```

1. 566
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SYNOV2000476"
/tissue_type="synovial membrane tissue from rheumatoid
arthritis"
/clone_1b="SYNOV2"
/notes="Vector: pME18SFL3"

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ORIGIN

Alignment Scores:

Pred. No.: 1, 03e-44 Length: 566
 Score: 509.00 Matches: 95
 Percent Similarity: 91.9% Conservative: 7
 Best Local Similarity: 85.6% Mismatches: 9
 Query Match: 86.6% Indels: 0
 DB: 9 Gaps: 0

US-10-092-640-36 (1-111) x DA971136 (1-566)

```

QY 1 GlnSerValleuthThgInpProSerValSerAlaAlaProGlyGlnValThrIle 20
DB 105 CAGTCTGTGCTGACTCAGCCACCTCAGCGTGGAGCCCGGAGAGGATCACCATC 164
QY 21 SerCysSerGlySerSerSerAniIleGlyAsnAsnTyValSerTrpTyrgInGlnIleu 40
DB 165 TCTTGTTCGGAAGCACTCCAACTCGGAAGTAACATGTATACCTGGTCCGCAATTC 224
QY 41 ProGlyThrAlaProlybLeuLeuIleTyrgLysIleThrAsnArgProAlaGlyValPro 60
DB 225 CCAAGAACCGCCCCCAAACTCTCATCTTATAGAAATATAGAGGCGCTTAGGGATCCCT 264
QY 61 AspArgPheSerGlySerIlySerGlyThnSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 285 GACCGATCTCTGGCTCCAACTCTGACCTGACCTCCCTGACATCAGTGGGCTCCAG 344
QY 81 SerGluAspGluAlaAspTrpTyrgAlaAlaIleTrpAspAspSerLeuSerGlyTrpVal 100

```

```

Db      345  TCTGAGGATGAGCGCTGATTATTACTGTGACGCTTGAGGACAGCTGAAATGATTGGGTG 404
      |||
Qy      101  Phegiylgylgylthrlsleuthrvalleugly 111
      |||
Db      405  TTCGGCGGAGGAGCAAGCTGACCGCTCCAGGT 437
      |||

RESULT 12
LOCUS   DA920210      578 bp      mRNA      linear      EST 03-DEC-2005
DEFINITION DA920210 SMINT2 Homo sapiens cDNA clone SMINT2005585 5', mRNA
sequence.
ACCESSION DA920210
VERSION   DA920210.1 GI:83074499
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homiidae; Homo.
REFERENCE 1 (bases 1 to 578)
AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
           Yamashita,R., Yamamoto,U., Sekine,M., Tsuritani,K., Wakaquri,H.,
           Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
           Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
           Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
           Tanabe,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
           Diversification of Transcriptional Modulation: Large-scale
           Identification and Characterization of Putative Alternative
           Promoters of Human Genes
JOURNAL   Genome Res. 16 (1), 55-65 (2006)
COMMENT   1634560
           Contact: Takao Isogai
           FLJ Project (HRI Team)
           Helix Research Institute
           2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
           Tel: 81-438-52-3975
           Fax: 81-438-52-3986
           Email: flj-cdna@nifty.com
           NEDO human cDNA project (New Energy and Industrial Technology
           Developmental Organization, Japan); cDNA library construction:
           Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
           Research Association for Biotechnology (RAB) and Biotechnology
           Center, National Institute of Technology and Evaluation; 3'-end one
           pass sequencing: RAB.
FEATURES
         source             1..578
         location/Qualifiers
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="SMINT2005585"
         /issue_type="small intestine"
         /clone_lib="SMINT2"
         /note="Vector: pME18SFL3"

ALIGNMENT Scores:
Pred. No.:      1.06e-44      Length:      578
Score:          509.00      Matches:      97
Percent Similarity: 91.0%      Conservative: 4
Best Local Similarity: 87.4%      Mismatches: 10
Query Match:    86.6%      Indels:      0
DB:            9      Gaps:      0

US-10-092-640-36 (1-111) x DA920210 (1-578)

Qy      1  GlnSerValleuThrgInPrProSeValSerAlaAlaProGlyGlnInyValThrIle 20
      |||
Db      102  CAGTGTGTCTACTACAGCCACCTCTAGGCTCTGGAGACCCCGGCGAGGGGTCCACATC 161
      |||
Qy      21  SerCySerGlySerSerSerAnillegIyaAnsnrYrValSerTrpYrGlnGlnleu 40
      |||
Db      162  TCTGTGTTGGAGAGCTCCAAACATCGGAATAATATATGTACTGTGTACAGCAATCTC 221
      |||

```

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Qy      41  ProGlyThrAlaProIlyleuLeuIleTyrglyhiIsthrAsnArgProAlaIlyValPro 60
      |||
Db      222  CCAGAGAGGCGCCCGCCAAACTCCTCATCTATATAGATCAAGCGGCGCTGCTCCT 281
      |||
Qy      61  AspArgPheSerGlySerIlySerGlyThrsSerAlaSerIleValIleSerGlyPheArg 80
      |||
Db      282  GACCATTTCTCTGGCTCCAGCTCTGGACCTCAGCTCCCTGGCCATCATGTGGCTCCGG 341
      |||
Qy      81  SerGluAepGluAlaAspTrpYrCyAlaAlaIrtPaSpAspSerIleuSerGlyTrpVal 100
      |||
Db      342  TCCGAGGATGAGGCTAATATTACTGTGCAGATGAGATGACAGCTGACTGTGTGGTG 401
      |||
Qy      101  Phegiylgylgylthrlsleuthrvalleugly 111
      |||
Db      402  TTCGGCGGAGGAGCAAGCTGACGCTCCTCGGT 434
      |||

RESULT 13
LOCUS   DN998001      620 bp      mRNA      linear      EST 17-MAY-2005
DEFINITION TC103037 Human breast cancer tissue, large insert, pCMV expression
library Homo sapiens cDNA clone TC103037 5', similar to Homo
sapiens, clone WGC:32654 IMAGE:4701898, complete cds, mRNA
sequence.
ACCESSION DN998001
VERSION   DN998001.1 GI:66257828
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homiidae; Homo.
REFERENCE 1 (bases 1 to 620)
AUTHORS   Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
           Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
           Zhang,X., Jay,G. and He,W.
           High-throughput cloning of full-length human cDNAs directly from
           cDNA libraries optimized for large and rare transcripts
JOURNAL   Unpublished (2005)
COMMENT   Contact: Kovacs, KP
           High Throughput cDNA Cloning
           Origene Technologies, Inc. ( www.origene.com )
           6 Taft Court, Suite 100, Rockville, MD 20850, USA
           Tel: 301 340 3188
           Fax: 301 340 8606
           Email: cDNA@origene.com
           This EST submission is part of an on-going human full-length
           cloning project at Origene Technologies, Inc.
           Please contact Origene for access.
           Origene Technologies, Inc.
           6 Taft Ct. Suite 100
           Rockville, MD 20850
           Tel: (301) 340-3188
           http://www.origene.com
           Seq primer: pCMV6 Spriime forward vector primer, Origene
           Technologies Inc.
FEATURES
         source             1..620
         location/Qualifiers
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="TC103037"
         /issue_type="breast cancer"
         /clone_lib="Human breast cancer tissue, large insert, pCMV
         expression library"
         /note="Organ: Mammary gland (cancer tissue); Vector:
         pCMV6-Xb5; Site 1: EcoRI; Site 2: XhoI/Sall compatible end
         ligatio; Oligo-dT primed reverse transcription optimized
         for large and GC rich mRNA transcripts, cDNA size
         selection, optimized ligation for large inserts into
         mammalian expression vector, random clones selected for
         end sequence verification of full-length genes"

ORIGIN

```

Alignment Scores:

Pred. No.: 1.16e-44 Length: 620
 Score: 509.00 Matches: 95
 Percent Similarity: 91.9% Conservative: 7
 Best Local Similarity: 85.6% Mismatches: 9
 Query Match: 86.6% Indels: 0
 DB: 9 Gaps: 0

US-10-092-640-36 (1-111) x DN998001 (1-620)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIle 20
 |||||
 DB 91 CAGTCTGTCTGACTACGCCACCTTCAGCTCTGGAGCCCGGAGGAGGTCACCATC 150
 |||||
 QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
 |||||
 DB 151 TCTTGTCTTGGAGAGAGCTCCGACATCGAAGTAATATGTAATGTTCCAGCAGCTC 210
 |||||
 QY 41 ProGlyThrAlaProIleuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro 60
 |||||
 DB 211 CCGAGAACGGCCCCCAAACTCCATCTATAGAAATATATCATGAGGAGGAGGTCCT 270
 |||||
 QY 61 AspArgPheSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 80
 |||||
 DB 271 GACCGATTCTCTGGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAG 330
 |||||
 QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaAlaTyrAspAspSerLeuSerGlyTyrVal 100
 |||||
 DB 331 TCCGAGATGAGGCTGATTTATTTCTGTGATCATGAGATGACAGCTGAGTGGCTGGTG 390
 |||||
 QY 101 PheGlyGlyGlyThrIleLeuThrValLeuGly 111
 |||||
 DB 391 TTCGGCGAGGAGGACCAAGCTGACCTCTAGGT 423

RESULT 14

BG745508

LOCUS 602724089F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4850231 5',

DEFINITION mRNA sequence.

ACCESSION BG745508

VERSION BG745508.1 GI:14056161

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 680)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: L16M1691 row: b column: 24

High quality sequence stop: 678.

Location/Qualifiers

1. 680

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4850231"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 113"

/note="Organ: spleen; Vector: pOMB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned

ORIGIN

into EcoRI/XhoI sites using the following 5' adaptor:
 GGCCAGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

Alignment Scores:

Pred. No.: 1.31e-44 Length: 680
 Score: 509.00 Matches: 97
 Percent Similarity: 90.1% Conservative: 3
 Best Local Similarity: 87.4% Mismatches: 11
 Query Match: 86.6% Indels: 0
 DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x BG745508 (1-680)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIle 20
 |||||
 DB 89 CAGTCTGTCTGACTACGCCACCTTCAGCTCTGGAGCTCCGGAGGAGGTCACCATC 148
 |||||
 QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
 |||||
 DB 149 TCTTGTCTTGGAGAGAGCTCCACATCGAATTAATTAATTAATTAATTAATTAATTA 208
 |||||
 QY 41 ProGlyThrAlaProIleuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro 60
 |||||
 DB 209 CCGAGAACGGCCCCCAAACTCCATCTATAGAAATATATCATGAGGAGGAGGTCCT 268
 |||||
 QY 61 AspArgPheSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 80
 |||||
 DB 269 GACCGATTCTCTGGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAG 328
 |||||
 QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaAlaTyrAspAspSerLeuSerGlyTyrVal 100
 |||||
 DB 329 TCCGAGATGAGGCTGATTTATTTCTGTGATCATGAGATGACAGCTGAGTGGCTGGTG 388
 |||||
 QY 101 PheGlyGlyGlyThrIleLeuThrValLeuGly 111
 |||||
 DB 389 TTCGGCGAGGAGGACCAAGCTGACCTCTAGGT 421

RESULT 15

AM405612

LOCUS 498 bp mRNA linear EST 16-FEB-2000

DEFINITION UI-HF-BL0-abs-b-11-0-UI.r1 NIH MGC_37 Homo sapiens cDNA clone

IMAGE:3057381 5', mRNA sequence.

ACCESSION AM405612

VERSION AM405612.1 GI:6924669

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 498)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www.bio.llnl.gov/dbp/image/image.html

Seq primer: M13 Forward.

Location/Qualifiers

1. 498

/organism="Homo sapiens"

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 17:06:37 ; Search time 144.3 Seconds
(without alignments)
2158.972 Million cell updates/sec

Title: US-10-092-640-36

Perfect score: 588
Sequence: 1 QSVITQPPVSAAPGQKVTI.....WDSLSGWVFGSGTKTVLG 111

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+.p2n.model -DEV=xlh
-Q/abses/ABSSMBE.spool/US10092640/runat.25052006.155719.5922/app.query.fasta_1
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALL=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MAXLEN=2000000000
-HOST=abs02n -USER=US10092640@CGN 1 1 252 @runat.25052006.155719.5922
-NCPu=6 -ICPU=3 -NO MAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	588	100.0	774	2	US-08-665-202-4
2	588	100.0	774	3	US-09-315-574-4
3	516	87.8	908	3	US-09-273-839A-9
4	508	86.4	327	3	US-09-240-274-128
5	508	86.4	327	3	US-09-240-274-128
6	504	85.7	333	3	US-09-848-798-128
7	486	82.7	333	2	US-08-264-093-5
8	486	82.7	333	2	US-08-477-553A-43

9	480	81.6	327	3	US-09-240-274-129	Sequence 129, App
10	480	81.6	327	3	US-09-848-798-129	Sequence 129, App
11	477.5	81.2	326	2	US-08-345-321-3	Sequence 3, App1
12	477.5	81.2	935	2	US-09-049-672A-20	Sequence 20, App1
13	476	81.0	327	3	US-09-240-274-124	Sequence 124, App
14	476	81.0	327	3	US-09-848-798-124	Sequence 124, App
15	476	81.0	705	3	US-09-372-425A-3	Sequence 3, App1
16	471	80.1	327	3	US-09-240-274-130	Sequence 130, App
17	471	80.1	327	3	US-09-848-798-130	Sequence 130, App
18	471	80.1	585	3	US-09-620-312D-551	Sequence 551, App
19	469	79.8	327	3	US-09-240-274-126	Sequence 126, App
20	469	79.8	327	3	US-09-848-798-126	Sequence 126, App
21	468	79.6	327	3	US-09-240-274-131	Sequence 131, App
22	468	79.6	327	3	US-09-848-798-131	Sequence 131, App
23	466	79.3	326	3	US-10-153-437-2	Sequence 2, App1
24	466	79.3	895	3	US-09-049-672A-25	Sequence 25, App1
25	466	79.3	5079	3	US-09-809-517A-41	Sequence 41, App1
26	465	79.1	330	2	US-08-199-911-1	Sequence 1, App1
27	463	78.7	915	4	US-09-880-107-3743	Sequence 3743, App
28	462	78.6	333	2	US-08-652-816A-27	Sequence 27, App1
29	458	77.9	774	5	US-10-072-301A-26	Sequence 26, App1
30	457.5	77.8	333	2	US-08-305-683A-3	Sequence 3, App1
31	454	77.2	327	3	US-09-025-769B-50	Sequence 50, App1
32	454	77.2	327	3	US-09-490-070A-50	Sequence 50, App1
33	454	77.2	327	3	US-09-490-153-50	Sequence 50, App1
34	454	77.2	327	3	US-09-490-324-50	Sequence 50, App1
35	451.5	76.8	933	3	US-09-079-029-8	Sequence 8, App1
36	450	76.5	327	3	US-09-240-274-223	Sequence 223, App
37	450	76.5	327	3	US-09-848-798-223	Sequence 223, App
38	446.5	75.9	1005	3	US-09-646-028-41	Sequence 41, App1
39	446.5	75.9	1020	3	US-09-646-028-47	Sequence 47, App1
40	446.5	75.9	1047	3	US-09-646-028-44	Sequence 44, App1
41	445	75.7	327	3	US-09-240-274-125	Sequence 125, App
42	445	75.7	327	3	US-09-848-798-125	Sequence 125, App
43	444.5	75.6	330	3	US-09-240-274-132	Sequence 132, App
44	444.5	75.6	330	3	US-09-848-798-132	Sequence 132, App
45	440	74.8	327	3	US-09-240-274-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-08-665-202-4
; Sequence 4, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995

```
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..774
OTHER INFORMATION: /note="sequence of C6 sfv
OTHER INFORMATION: antibody C6.5"
US-08-665-202-4

Alignment Scores:
Pred. No.: 7,98e-58 Length: 774
Score: 588.00 Matches: 111
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x US-08-665-202-4 (1-774)
QY 1 GlnSerValIleuThrGlnProProSerValSerAlaAlaProGlyGlnIleValThrIle 20
DB 433 CAGTCTGTGTTACGAGCGCCCTCAGTCTGCGGCCCGAGACAGAGGTCAACCATC 492
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 493 TCCTGCTCTGGAAGAGCGCTCAACATTTGGGAATTAATTAATTAATTAATTAATTA 552
QY 41 ProGlyThrAlaProIleuLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 60
DB 553 CCAGGAAACAGCCCGCAACCTCTCATCTATGTGTACACCAATCGGCGCGAGGTCCCT 612
QY 61 AspArgPheSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 80
DB 613 GACCATTTCTGCTGCTCCAGTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 672
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleuAspAspSerIleuSerGlyTyr 100
DB 673 TCCGAGATGAGGCTGATTATTAATGTCAGCATGGGATGACAGCTGAGTGGTGGGTG 732
QY 101 PheGlyGlyGlyThrIleuLeuThrValIleuGly 111
DB 733 TTCGGCGAGGAGGACCAAGCTGACCGTCTAGGT 765

RESULT 2
US-09-315-574-4
Sequence 4, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..774
OTHER INFORMATION: /note="sequence of C6 sfv
OTHER INFORMATION: antibody C6.5"
US-09-315-574-4

Alignment Scores:
Pred. No.: 7,98e-58 Length: 774
Score: 588.00 Matches: 111
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-36 (1-111) x US-09-315-574-4 (1-774)
QY 1 GlnSerValIleuThrGlnProProSerValSerAlaAlaProGlyGlnIleValThrIle 20
DB 433 CAGTCTGTGTTACGAGCGCCCTCAGTCTGCGGCCCGAGACAGAGGTCAACCATC 492
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 493 TCCTGCTCTGGAAGAGCGCTCAACATTTGGGAATTAATTAATTAATTAATTAATTA 552
QY 41 ProGlyThrAlaProIleuLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 60
DB 553 CCAGGAAACAGCCCGCAACCTCTCATCTATGTGTACACCAATCGGCGCGAGGTCCCT 612
QY 61 AspArgPheSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 80
DB 613 GACCATTTCTGCTGCTCCAGTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 672
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleuAspAspSerIleuSerGlyTyr 100
DB 673 TCCGAGATGAGGCTGATTATTAATGTCAGCATGGGATGACAGCTGAGTGGTGGGTG 732
QY 101 PheGlyGlyGlyThrIleuLeuThrValIleuGly 111
DB 733 TTCGGCGAGGAGGACCAAGCTGACCGTCTAGGT 765

RESULT 3
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```
US-09-273-839A-9
; Sequence 9, Application US/09273839A
; Patent No. 6329156
; GENERAL INFORMATION:
; APPLICANT: Cixino, Nick M
; APPLICANT: Jackson, Paul J
; APPLICANT: Lehnert, Bruce E
; TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface
; FILE REFERENCE: S-89,662
; CURRENT APPLICATION NUMBER: US/09/273,839A
; CURRENT FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-273-839A-9

Alignment Scores:
Pred. No.: 1,63e-49 Length: 908
Score: 516.00 Matches: 98
Percent Similarity: 93.7% Conservative: 6
Best Local Similarity: 88.3% Mismatches: 7
Query Match: 87.8% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-36 (1-111) x US-09-273-839A-9 (1-908)

QY 1 GlnSerValLeuThrGlnProPheSerValSerAlaAlaProGlyGlnValThrIle 20
DB 505 CAGTCGTGTGACGACCGCCCTCAGCCTCGGAGACCCCGGAGAGAGGTCCACCATC 564
QY 21 SerCysSerGlySerSerSerSerAlaIleGlyAsnAsnTyValSerTrpTyGlnGlnLeu 40
DB 565 TCTGTGTTGGAGAGCAGCTCCACATCGAAGATATTCCTTAACGTGATCCGACAGCTC 624
QY 41 ProGlyThrAlaProIleuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro 60
DB 625 CCAAGGAAACCGCCCAACTCCCTCATCTATAGTAACAGCAATCGCCCTCAGGGGTCCCT 684
QY 61 AspArgPheSerGlySerIleSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 685 GACCGATCTCTGGCTCCAAAGTCTGGACCTCAGCCCTCCCTGACATCAGTGGGCTCCG 744
QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaIlePheAspSerLeuSerGlyTrpVal 100
DB 745 TCCGAGGATGAGGCTGATTAATTAATCTGACGATGGGATGACAGCTGAGTGTGGGTG 804
QY 101 PheGlyGlyGlyThrIleLeuThrValIleGly 111
DB 805 TTCGGCGGAGGAGCCAAAGCTGACCGCTCAGGT 837

RESULT 4
US-09-240-274-128
; Sequence 128, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 128
; LENGTH: 327
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain M02
US-09-240-274-128

Alignment Scores:
Pred. No.: 3,27e-49 Length: 327
Score: 508.00 Matches: 95
Percent Similarity: 92.5% Conservative: 4
Best Local Similarity: 88.8% Mismatches: 8
Query Match: 86.4% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-36 (1-111) x US-09-240-274-128 (1-327)

QY 4 LeuThrGlnProPheSerValSerAlaAlaProGlyGlnValThrIleSerCysSer 23
DB 7 CTCACGACGCCGCCCTCAGCGTGGAGACCCCGGAGAGGTCCACCATCTTGTTC 66
QY 24 GlySerSerSerSerAlaIleGlyAsnAsnTyValSerTrpTyGlnGlnLeuProGlyThr 43
DB 67 GGAAGCAGCTCCCAACATCGAAGATATTAATGATTTGATACAGCAGCTCCAGAGAAC 126
QY 44 AlaProIleuLeuIleTyGlyHisThrAsnArgProAlaGlyValProAspArgPhe 63
DB 127 GCCCCCAACTCCTCATTAAGAAATATACACGCCCTCAGGGGTCCCTGACCAATTC 186
QY 64 SerGlySerIleSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArgSerGluAsp 83
DB 187 TCTGGCTCCAAAGTCTGGACCTCAGCCTCCCTGACATCAGTGGCTCCGATCCAGAGAT 246
QY 84 GluAlaAspTyTyTyCysAlaAlaIlePheAspSerLeuSerGlyTrpValPheGly 103
DB 247 GAGGCTGATTAATTAATCTGACGATGAGATGACAGCTGATGTTGGGTTCGGCGGA 306
QY 104 GlyThrIleLeuThrValIleu 110
DB 307 GGGACCAAGCTGACCGTCTTA 327

RESULT 5
US-09-848-798-128
; Sequence 128, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 128
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain M02
US-09-848-798-128

Alignment Scores:
Pred. No.: 3,27e-49 Length: 327
Score: 508.00 Matches: 95
Percent Similarity: 92.5% Conservative: 4
Best Local Similarity: 88.8% Mismatches: 8
Query Match: 86.4% Indels: 0
DB: 3 Gaps: 0
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US-10-092-640-36 (1-111) x US-09-848-798-128 (1-327)

QY	4	LeuThgIlnProPseValSerAlaAlaProGlyGlnValThrIleSerCysSer	23
Db	7	CTCAGCAGCCGCCCTCACGCTCGGGACCCCGGGACAGAGGTGCACATCTCTGTTC	66
QY	24	GlySerSerSerAsnIleGlyAsnIleValSerTyrGlnGlnLeuProGlyThr	43
Db	67	GGAGAGAGCTCCAAACATCGAAGTAATTATGTATTTGGTCCAGCACTCCCGAGAACG	126
QY	44	AlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValProAspArgPhe	63
Db	127	GCCCCCAAACCTCTCATCTATAGAAATATATCAGCGGCCCTCAGGGGTCCCGACGATTC	186
QY	64	SerGlySerIlySerSerIlyThrSerAlaSerLeuAlaIleSerGlyPheArgSerGluAsp	83
Db	187	TCGTGGCTCCAAAGTCGTGGACCTCAGCTCCCTGGCCATCAGGGGCTCCGGTCCGAGGAT	246
QY	84	GluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerGlyTyrValPheGlyGly	103
Db	247	GAGCGTGAATTATTAAGTCGTGCAGCATGGATGACACGCTGAGGTGGGTCTTCGGCGGA	306
QY	104	GlyThrIlyLeuThrValLeu	110
Db	307	GGGACCAAGCTGACCGGTCTCA	327

RESULT 6

Sequence 7, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-SP11A RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 333
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(333)
OTHER INFORMATION:
US-09-424-840B-7

Alignment Scores:

Pred. No.:	9.6e-49	Length:	333
Score:	504.00	Matches:	93
Percent Similarity:	92.7%	Conservative:	8
Best Local Similarity:	85.3%	Mismatches:	8
Query Match:	85.7%	Indels:	0
DB:	3	Gaps:	0

QY	3	ValLeuThrcInGlnProSerValSerAlaAlaProGlyGlnValThrlLSecCys	22
QY	1	GTGATGACTCAGGCACCTCCTAGCGTCTGGAGACCCCGGAGAGGTCACCATCTCTTGT	60
Db	1	GTGATGACTCAGGCACCTCCTAGCGTCTGGAGACCCCGGAGAGGTCACCATCTCTTGT	60
QY	23	SeerGlySerSerSerSerLniLcGlyAsnAsnTrpValSerTrpTrpGlnGlnLeuProGly	42
Db	61	TCGGAGAGCGCTCCCAACATCGGAAATAATCTGTAACCTGGATACCCACACTCCCGAGA	120

Oy	43	ThrlaPProlysleuLeuLlETyGlyYlshTrnaAAGProlAGlYalProbaPAG	62
	121	ACGGCCCCCAACTCTCATCTATAGTAATATACGGCGCCCTCAGGGGTCCCTGACCA	180
Oy	63	PheserGlySerIySserGlyYThSerAlaSerLeuAlaIleSerGlyPheargSerGlu	82
	181	TTCTCTGGCTCCAGTGTGGACCTCAGCTCTCCCTGGCCATCAGTGGGCTCCAGTGTGAG	240
Oy	83	AspGluAlaApPlyTTrYrCyAlaAlaTrpPheAppSerLeuSerGlyTTrpValPheGly	102
	241	GATAGGCTGATTrTTrTACTGTGCAGCAAGGATGACACCTGAAAGTGGGTGTTCGGGC	300
Oy	103	GIyGlyThrlYsleuThrValIleGly	111
	301	GGAGGGACCAAGCTGACCCGTCTAGCT	327

RESULT 7

Sequence 5, Application US/08264093
Patent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Aделаide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 866-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-264-093-5

Alignment Scores:

Pred. No.:	1,09e+46	Length:	33
Score:	486.00	Matches:	92
Percent Similarity:	89.2%	Conservative:	7
Best Local Similarity:	82.9%	Mismatches:	12
Query Match:	82.7%	Indels:	0
DB:	2	Gaps:	0

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Oy      1 GlnserValIeuThrGlnProPseRvaIsRaIalaProGlyGlnLysValThrIle 20
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Db      1 CAGTGTGTGCTCAGCCACCTTCAGCGTCTGGAGACCCCCGGGCAGAGGGTCAACATC 60
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Db 127 GCCCCAAACCTCCTATCTATAGATATACAGCGGCGCTCAGGGGTCCCTGACGCGATTC 186
Qy 64 SerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArgSerGluAsp 83
Db 187 TCTGCTCCAAAGTCGGACCTCAGCCTCCCTGGCCATCAGGGGCTCCGCTCCGAGGCT 246
Qy 84 GUAAlaAspIyrTyrcysAlaAlaIrrPaAspSerLeuSerGlyTrrpValPheGlyGly 103
Db 247 GAGGCTGATTATTACTGTCGGCATGCGATGACAGCTTACGCTGATTCGGCGGA 306
Qy 104 GlyThrIysLeuThrValleu 110
Db 307 GGGACCAACTGACCGTCTTA 327

RESULT 10
US-09-848-798-129
; Sequence 129, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RHD)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain M03
US-09-848-798-129

Alignment Scores:
Pred. No.: 5,12e-46 Length: 327
Score: 480.00 Matches: 92
Percent Similarity: 89.7% Conservative: 4
Best Local Similarity: 86.0% Mismatches: 11
Query Match: 81.6% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-36 (1-111) x US-09-848-798-129 (1-327)

Qy 4 LeuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIleSerCysSer 23
Db 7 CTCACCTCAGCCACCTCCTCAGCGCTGAGACCCCGGCAAGGCTCCACCTCTCTGTTCT 66
Qy 24 GlySerSerSerAsnIleGlyAsnAsnIyrValSerTrrpYrGlnGlnLeuProGlyThr 43
Db 67 GGAAGCAGCTCCAACTCGAAGTATATGATATCTGATGACAGCAGCTCCAGGAACG 126
Qy 44 AlaProIysLeuLeuIleTyrcysAlaAlaIrrPaAspSerLeuSerGlyTrrpValPheGlyGly 63
Db 127 GCCCCAAACCTCCTATCTATAGATATACAGCGGCGCTCAGGGGTCCCTGACGCGATTC 186
Qy 64 SerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArgSerGluAsp 83
Db 187 TCTGCTCCAAAGTCGGACCTCAGCCTCCCTGGCCATCAGGGGCTCCGCTCCGAGGCT 246
Qy 84 GUAAlaAspIyrTyrcysAlaAlaIrrPaAspSerLeuSerGlyTrrpValPheGlyGly 103
Db 247 GAGGCTGATTATTACTGTCGGCATGCGATGACAGCTTACGCTGATTCGGCGGA 306
Qy 104 GlyThrIysLeuThrValleu 110
Db 307 GGGACCAACTGACCGTCTTA 327

RESULT 11
US-08-345-321-3
; Sequence 3, Application US/08345321
; Patent No. 5914109
; GENERAL INFORMATION:
; APPLICANT: ZOLLA-PAZNER, Susan
; APPLICANT: GORNY, Mirosław K.
; TITLE OF INVENTION: HETEROHYBRIDOMAS PRODUCING HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO HIV-1
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/345,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,675
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: ZOLLA-PAZNERIB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..396
US-08-345-321-3

Alignment Scores:
Pred. No.: 1,29e-45 Length: 396
Score: 477.50 Matches: 90
Percent Similarity: 86.3% Conservative: 8
Best Local Similarity: 81.1% Mismatches: 12
Query Match: 81.2% Indels: 1
DB: 2 Gaps: 1

US-10-092-640-36 (1-111) x US-08-345-321-3 (1-396)

Qy 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIle 20
Db 58 CAGTCTGTTGATACGACGCGGCTCAGTGTCTGCGGCCCGAGAGAGGTCCACCATTC 117
Qy 21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnIyrValSerTrrpYrGlnGlnLeu 40
Db 118 TCTCTCTCTGGAAGCAGCTCCAACTCCCAATATATGATATCTGATGACAGCAGATTC 177
Qy 41 ProGlyThrAlaProIysLeuLeuIleTyrcysAlaAlaIrrPaAspSerLeuSerGlyTrrpValPheGlyGly 60
Db 178 CAGGAACAGGCCCCAAACTCCTCATTTATGCAATATAGCGACCTCCAGGATTCCT 237
Qy 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80

Db 238 GACCATTCCTGCTCCCAAGTCGACGATCAGCCCTGGGACATCAGCAGCTCCAG 297
 QY 81 SerGlaaspGluAlaapTyTYrCYsAlaAlaTTPaspaspSerleuSergly---Tyr 99
 Db 298 ACTGGGAGACAGCCCATTTATTTCTGCGCAACATGGGATAGCGCCCTGAGTGTG 357
 QY 100 ValPheGlyGlyGlyThyLeuThrValleu 110
 Db 358 GTTTCGGCGAGGAGCAACAGTGCCTGCTCTTA 390

RESULT 12
 US-09-049-672A-20
 ; Sequence 20, Application US/09049672A
 ; Patent No. 6135941
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Baughn, Mariah R.
 ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/049,672A
 ; FILING DATE: HERewith
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ceirone, Michael C
 ; REGISTRATION NUMBER: 39,132
 ; REFERENCE/DOCKET NUMBER: PF-0497 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 935 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: ADREUT05
 ; CLONE: 2492122
 ; US-09-049-672A-20

Alignment Scores:
 Pred. No.: 4.17e-45 Length: 935
 Score: 477.50 Matches: 93
 Percent Similarity: 90.2% Conservative: 8
 Best Local Similarity: 83.0% Mismatches: 10
 Query Match: 81.2% Indels: 1
 DB: 3 Gaps: 1

US-10-092-640-36 (1-111) x US-09-049-672A-20 (1-935)

QY 1 GlnSerValleuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
 Db 131 CAGTCTGTGTGACGAGCGCCCTCAGTCTGGGGCCCGAGGAGGATCCATC 190
 QY 21 SerCySerGlySerSerSerSerAlaIleGlyAsnAsnTyr---ValSerTTPYrGlnGln 39
 Db 191 TCCTGCACGTGGGAGCAGCTCCAACTCGGGGAGGTTATATATACCTGATCAGTACAG 250
 QY 40 LeuProGlyThrAlaProLysLeuLeuIleTyGlyHisThrAsnArgProAlaGlyVal 59
 Db 251 CTCACGAAACAGCCCCCAAACTCCATCATGTATAGTAAATGGCCCTCAGGGGTC 310
 QY 60 ProAspArgPheSerGlySerGlySerGlyThrSerAlaSerLeuAlaIleSerglyPhe 79
 Db 311 CTGACCGATTCCTGCTCCCAAGTCGACCTCAGCCCTCCCTGGCCATCAGTGGGCTC 370
 QY 80 ArgSerGluaspGluAlaapTyTYrCYsAlaAlaTTPaspaspSerleuSerglyTyr 99
 Db 371 CAGGCTGAGGATGAGGCTGATTTATCTGCACTCTTATGACAGCAGCTGAGTGTGTG 430
 QY 100 ValPheGlyGlyGlyThyLeuThrValleuGly 111
 Db 431 GTATTCGGCGAGGAGCAACAGTGCCTGCTCTT 466

RESULT 13
 US-09-240-274-124
 ; Sequence 124, Application US/09240274
 ; Patent No. 6255455
 ; GENERAL INFORMATION:
 ; APPLICANT: Siegel, Donald L.
 ; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 ; FILE REFERENCE: 09596-42U2
 ; CURRENT APPLICATION NUMBER: US/09/240,274
 ; EARLIER FILING DATE: 1999-01-29
 ; EARLIER APPLICATION NUMBER: 60/081,380
 ; EARLIER FILING DATE: 1998-04-10
 ; EARLIER APPLICATION NUMBER: 60/028,550
 ; EARLIER FILING DATE: 1996-10-11
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 124
 ; LENGTH: 327
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: anti-Rh(D) chain L03
 ; US-09-240-274-124

Alignment Scores:
 Pred. No.: 1.47e-45 Length: 327
 Score: 476.00 Matches: 91
 Percent Similarity: 89.7% Conservative: 5
 Best Local Similarity: 85.0% Mismatches: 11
 Query Match: 81.0% Indels: 0
 DB: 3 Gaps: 0

US-10-092-640-36 (1-111) x US-09-240-274-124 (1-327)

QY 4 LeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIleSerglySer 23
 Db 7 CTCACGAAACAGCCCCCAAACTCCATCATGTATAGTAAATGGCCCTCAGGGGTC 66
 QY 24 GlySerSerSerAsnIleGlyAsnAsnTyValSerTTPYrGlnGlnLeuProGlyTyr 43
 Db 67 GGCAGAGCTCCAACTCGGAATATATCTGTAAGTGTATACCACTCCAGGAATG 126
 QY 44 AlaProLysLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValProAspArgPhe 63
 Db 127 GCCCCCAACTCCTCATCTATCTATATGATGTCAGCGGCCCTCAGGGGCTCCTGACCATTC 186
 QY 64 SerGlySerTySerGlyThrSerAlaSerLeuAlaIleSerglyPheArgSerglyuasp 83

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Db 187 TCTGGCTCCAGTCTGGACCTCCTGGCCATCATGAGGGCCCTCCAGTCTGAGAT 246
QY 84 GIUAIAASPTTYTCYSAIAAATPASPASPSeuSerGlyTyrValPheGlyGly 103
Db 247 GAGGCTGATTAATATGTCAGACATGACAGCCTTAATGTCGGGTTCCGGCGGA 306
QY 104 GIYThrLysLeuThrValLeu 110
Db 307 GGGACCAAGCTGACCTCTCTC 327

RESULT 14
US-09-848-798-124
; Sequence 124, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain L03
US-09-848-798-124

Alignment Scores:
Pred. No.: 1,47e-45 Length: 327
Score: 476.00 Matches: 91
Percent Similarity: 89.7% Conservatve: 5
Best Local Similarity: 85.0% Mismatches: 11
Query Match: 81.0% Indels: 0
Gaps: 0
DB: 3

US-10-092-640-36 (1-111) x US-09-848-798-124 (1-327)
QY 4 LeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIleSerCysSer 23
Db 7 CTCACCTCAGCCACCTCTGAGACCCCGGGGACAGGGGTACCATCTCTGTTCT 66
QY 24 GlysSerSerSerAsnIleGlyAsnAsnTyrValSerTyrTyrGlnGlnLeuProGlyThr 43
Db 67 GGCAGTAGCTCCACATCGGAAATATCATGTAGAGTGTACAGCACTCCAGAGAAATG 126
QY 44 AlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValProAspArgPhe 63
Db 127 GCCCCAAACTCCTCATCTAATCTAATGTCAGCGGCTCCAGGGGTCCCTGACCGATTC 186
QY 64 SerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArgSerGluAsp 83
Db 187 TCTGGCTCCAAAGTCGACCTCAGCCTCCGCGCATGACGGGCTCCAGTCTAGAGAT 246
QY 84 GIUAIAASPTTYTCYSAIAAATPASPASPSeuSerLysSerGlyTyrValPheGlyGly 103
Db 247 GAGGCTGATTAATATGTCAGACATGACAGCCTTAATGTCGGGTTCCGGCGGA 306
QY 104 GIYThrLysLeuThrValLeu 110
Db 307 GGGACCAAGCTGACCTCTCTC 327

RESULT 15
US-09-372-425A-3
; Sequence 3, Application US/09372425A
; Patent No. 6475749
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; GENERAL INFORMATION:
; APPLICANT: Sherie L. Morrison
; APPLICANT: Ramon Montano
; TITLE OF INVENTION: Improved Rh Antibody
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Openheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,425A
; FILING DATE: August 11, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenakmp, David J.
; REGISTRATION NUMBER: 29,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 nucleotides
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Light chain - DNA
US-09-372-425A-3

Alignment Scores:
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Score: 476.00 Matches: 88
Percent Similarity: 88.3% Conservatve: 10
Best Local Similarity: 79.3% Mismatches: 13
Query Match: 81.0% Indels: 0
Gaps: 0
DB: 3

US-10-092-640-36 (1-111) x US-09-372-425A-3 (1-705)
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QY 21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTyrValSerTyrTyrGlnGlnLeu 40
Db 115 TCTGCTCTCGAAGAGAGCTCCACATCTGGAAATATTAATGATCTGTGTAACAGATTC 174
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
Db 175 CCAGGACAGCGCCCAACTTCTCATTTATGCAATATATCAAGCGACCTCCAGGGATTCCT 234
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db 225 GACCATTTCTCGGCTCCAAAGTCGACAGTCAGCCACCTGGGCATACCGGACTCCAG 294
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaATPASPASPSeuSerLysSerGlyTyrVal 100
Db 295 ACTGGGAGACGAGACCGGATTAATACGCGGAACATGAGATGACGCTGAGTCTGTGCTT 354
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
Db 355 TTCCGGCGGAGGAGCCGAAAGTAGACCTCTCTAGGT 387
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/ Fri May 26 08:42:23 2006

us-10-092-640-36.rni

Page 9

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: May 25, 2006, 20:50:52 ; Search time 1008.71 Seconds
(without alignments)
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Title: US-10-092-640-36

Perfect score: 588

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588	100.0	765	3	US-09-888-721-35 Sequence 35, Appl

2	566	96.3	807	3	US-09-888-721-37	Sequence 37, Appl
3	566	96.3	806	3	US-09-888-721-39	Sequence 39, Appl
4	566	96.3	861	3	US-09-888-721-41	Sequence 41, Appl
5	566	96.3	873	3	US-09-888-721-45	Sequence 45, Appl
6	566	96.3	888	3	US-09-888-721-43	Sequence 43, Appl
7	553	94.0	333	9	US-10-679-032-36	Sequence 36, Appl
8	545	92.7	333	9	US-10-679-032-6	Sequence 6, Appl
9	536	91.2	333	9	US-10-679-032-30	Sequence 30, Appl
10	533.5	90.7	336	9	US-10-679-032-2	Sequence 2, Appl
11	531	90.3	333	9	US-10-679-032-34	Sequence 34, Appl
12	529	90.0	333	9	US-10-679-032-38	Sequence 38, Appl
13	527	89.6	333	9	US-10-679-032-12	Sequence 12, Appl
14	525	89.3	333	9	US-10-679-032-18	Sequence 18, Appl
15	524.5	89.2	336	9	US-10-679-032-20	Sequence 20, Appl
16	521	88.6	333	9	US-10-679-032-28	Sequence 28, Appl
17	520	88.4	333	9	US-10-679-032-22	Sequence 22, Appl
18	517	87.9	732	8	US-10-779-461-87	Sequence 87, Appl
19	516	87.8	333	9	US-10-679-032-12	Sequence 12, Appl
20	516	87.8	744	9	US-10-800-023-18	Sequence 18, Appl
21	516	87.8	908	8	US-10-375-356A-9	Sequence 9, Appl
22	513	87.2	2635	6	US-10-198-846-13529	Sequence 13529, A
23	511	86.9	411	9	US-10-783-311-27	Sequence 27, Appl
24	510	86.7	333	9	US-10-679-032-24	Sequence 24, Appl
25	510	86.7	354	10	US-10-916-6758-28	Sequence 28, Appl
26	510	86.7	762	13	US-10-916-847-224	Sequence 24, App
27	508	86.4	327	3	US-09-848-798-128	Sequence 128, App
28	508	86.4	327	15	US-11-064-174-128	Sequence 128, App
29	507	86.2	328	9	US-10-679-032-26	Sequence 26, Appl
30	504	85.7	333	9	US-10-844-424-7	Sequence 7, Appl
31	503	85.5	768	3	US-09-747-669-4	Sequence 4, Appl
32	503	85.5	768	3	US-09-747-669-5	Sequence 5, Appl
33	503	85.5	768	6	US-10-290-703-4	Sequence 4, Appl
34	503	85.5	768	6	US-10-290-703-5	Sequence 5, Appl
35	502.5	85.5	441	10	US-09-988-115A-56	Sequence 56, Appl
36	502.5	85.5	441	10	US-10-705-519-56	Sequence 56, Appl
37	501	85.2	366	11	US-10-993-543-45	Sequence 45, Appl
38	500	85.0	333	9	US-10-679-032-32	Sequence 32, Appl
39	500	85.0	1640	6	US-10-198-846-13206	Sequence 13206, A
40	499	84.9	735	10	US-10-935-290-215	Sequence 215, App
41	499	84.9	780	10	US-10-935-290-213	Sequence 213, App
42	498	84.7	1565	6	US-10-198-846-13276	Sequence 13276, A
43	496	84.4	870	10	US-10-276-233A-4	Sequence 4, Appl
44	495	84.2	330	10	US-10-727-145-211	Sequence 211, App
45	495	84.2	366	11	US-10-993-543-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-888-721-35
Sequence 35, Application US/09888721
Patent No. US20020132990A1
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Wile, Pierre
APPLICANT: Zhu, Quan
APPLICANT: Laurent, Olivier
APPLICANT: Marasco, Wayne A.
APPLICANT: Scheman, Daniel
TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 765
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OY	21	SeRySSeRgIySeSeSeSeSaenIIeGlyAsnAspTyValSeTTPyYrGInGlnLeu	40
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OY	41	ProGlyYThrAlaProLyLeuLeuIIeTyYrGlyVHisThrAsnArgProAlaGlyValPro	60
Db	553	CCAGGAACAGCCCCCAAACTCCCACTATGATGACACCAACATGGCGGCGAGGGGTCCCT	612
OY	61	AspArgPheSeRgIySeRySSeRgIyThrSerAlaSerLeuAlaIleSeRgIyPheArg	80
Db	613	GACCGATTCTCTGGCTCCAAAGTGTGGACCTCAGCTCCTGGCCATCAATGGGTTCCGG	672
OY	81	SeRgIuAspGluAlaAspTyTyYrCyValAlaIleTPAspAspSeRleuSeRgIyTPVal	100
Db	673	TCCGAGGAGAGAGCTGATTATTACTGTGCTCCTGGGACATCAACCTCTCGGGCTGGGTG	732
OY	101	PheGlyGlyGlyThrIyLeuThrValIleuGly	111
Db	733	TTCCGCGGAGGAACCAAGCTGACCTGCTTAAGT	765

US-09-888-721-41
 Sequence 41, Application US/09888721
 Patent No. US20020132990A1
 GENERAL INFORMATION:
 APPLICANT: Huston, James S.
 APPLICANT: Wils, Pierre
 APPLICANT: Zhu, Quan
 APPLICANT: Laurent, Olivier
 APPLICANT: Marasco, Wayne A.
 APPLICANT: Scherman, Daniel
 TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
 TITLE OF INVENTION: DELIVERY
 FILE REFERENCE: 23611-A USA
 CURRENT APPLICATION NUMBER: US/09/888,721
 CURRENT FILING DATE: 2001-06-25
 PRIOR APPLICATION NUMBER: 60/213,653
 PRIOR FILING DATE: 2000-06-23
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 41
 LENGTH: 861
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Human/murine
 OTHER INFORMATION: chimeric single chain binding polypeptide
 OTHER INFORMATION: (G6M13-59Fv'-L2-KDEL)
 US-09-888-721-41

Alignment Scores:	
Pred. No.:	6, 2e-62
Score:	566.00
Percent Similarity:	98.2%
Best Local Similarity:	96.4%
Query Match:	96.3%
DB:	3
	Gaps: 0
	Matches: 861
	Conservative: 107
	Mismatches: 2
	Indels: 0
	Gaps: 0

US-10-0932-640-36 (1-111) x US-09-888-721-41 (1-861)

Qy	1	GlnSerValLeuThGlnProPheSerValSerAlaAlaProGlyGlnIysValThrIle	20
Db	433	CAGTCTGTGTTGACCGACCGCCCTCAGTCTCGCGGCCACGAGACGAGAGTCACCATC	492
Qy	21	SerCysSerGlySerSerSerSerAsnIleGlyAsnAsnTyValSerTrpTyArgGlnGlnLeu	40
Db	493	TCTCTCTCTGGAGACGCTCCAACTGGGAAATTAATGATATCTCGTATCCACGAGCTC	552
Qy	41	ProGlyThrAlaProIysLeuLeuIleTyArgIleHisThrAsnArgProAlaGlyValPro	60
Db	553	CCAGAAACAGCCCCCAATCTCTCATCTTATGATCAACCAATGAGGCCCGGAGGGTCCCT	612

Oy	61	AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaLleSergLYPheArg	80
Dd	613	GACCGATTCTTGAGTCCAAAGTCGTGGCACTAGCCTCCCTGGCATATGAGGGTTCCGG	672
Oy	81	SerGIuAspGluAlaAspTYrTYrCYsaLaalAtatPaSPasPserLeuSergLYTriPal	100
Dd	673	TCCGAGGATGASGCTATTATTACTGTGTGCTCTGGGACTACACCCTCTCGGGCTGGTG	732
Oy	101	PheGLYGLYGLYThrLYsLeuThrValLeuGLY	111
Dd	733	TTCCGGCGGAGAACCAAGCTGAACCGCTCAGGT	765

```

RESULT 5
US-09-888-721--45
; Sequence 45, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Schernan, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
US-09-888-721--45

```

Alignment Scores:	
Pred. No.:	6,31e-62
Score:	566.00
Percent Similarity:	98.2%
Best Local Similarity:	96.4%
Query Match:	96.3%
DB:	3
Length:	873
Matches:	1070
Conservative:	5
Mismatches:	2
Indels:	0
Gaps:	0

US-10-092-640-36 (1-111) x US-09-888-721-45 (1-873)	
Qy	1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnValValThrIle 20
Db	433 CAETCTGTGTATGACGACGCCCTCAGTGTCTGGGCCCAAGACAGAGAGTCAACATC 492
Qy	21 SerCysSerGlySerSerSerSerAsnIleGlyAsnAsnValValSerTyrGlyGlnLeu 40
Db	493 TCTGCTCTGGAAAGCAGCTCAACACTGGGAATATTTGTATCTGTGTACACACACTC 552
Qy	41 ProGlyThrAlaProIysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
Db	553 CCGAGAACAGCCCCCAACTCTCTCATATGATACACACCAATCGGCCCGAGGGGCTCCT 612
Qy	61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db	613 GACCGATTCTCTGGCTCCAAAGTCGTGGACCTCAGGCTCTCCGGGCATCAGTGGCTTCGGG 672
Qy	81 SerGlyAspGlyAlaAspTyrTyrCysAlaAlaIleTyrPaspAspSerLeuSerGlyTyrVal 100
Db	673 TCCGAGAGATGAGGCTGATTTATTAATCTGTGCTCTCGGACACACCTCTCGGGCTGGGTG 732
Qy	101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111

```

Db      733 TTCCGGGAGGAGCAAGCTGACCGTCTTAGGT 765
|||||
RESULT 6
US-09-888-721-43
; Sequence 43, Application US/09888721
; Patent No. US2002013290A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Schertman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
US-09-888-721-43

Alignment Scores:
Pred. No.:      6,45e-62      Length:      888
Score:          566.00       Matches:     107
Percent Similarity: 98.2%    Conservative: 2
Best Local Similarity: 96.4% Mismatches:    2
Query Match:    96.3%       Indels:      0
Db:              3          Gaps:         0

US-10-092-640-36 (1-111) x US-09-888-721-43 (1-888)
QY      1 GlnSerValIleuThrGlnProSerValSerAlaIleProGlyGlnIleValThrIle 20
      |||
Db      433 CAGTCTGTGTTACCGACGCGCCCTCAGTGTCTGCGGCCCGACAGACAGAGTCAACATC 492
QY      21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnIleValSerTrpIleGlnIleu 40
      |||
Db      493 TCCTGCTCTCGAAGCAGCTCCAACTGGGAAATTAATGATCTCGTACACGACGCTC 552
QY      41 ProGlyThrAlaProIleuIleuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
      |||
Db      553 CCAGAAACAGCCCCCAACTCCTCATGTATGATCAACCAATCGGCCCGACAGGGTCCCT 612
QY      61 AspArgPheSerGlySerIleSerGlyThrSerAlaSerIleAlaIleSerGlyPheArg 80
      |||
Db      613 GACCGATTCTCTGGCTCCAGTCTGGACCTCAAGCTCCCTGGCATTCAGTGGTTCCGG 672
QY      81 SerGluAspGluAlaAspTyrTrpCysAlaAlaIlePaspAspSerIleuSerGlyTrpVal 100
      |||
Db      673 TCCGAGGATGAGGCTGATTAATGCTGCTCCTGGGACTACACCTCTCGGGCTGGGTG 732
QY      101 PheGlyGlyGlyThrIleuThrValIleuGly 111
      |||
Db      733 TTCCGGGAGGAGCAACAGCTGACCGTCTTAGGT 765

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; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; TITLE OF INVENTION: TREATMENT OF ATHEROSCLEROSIS
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-36

Alignment Scores:
Pred. No.:      8,69e-61      Length:      333
Score:          553.00       Matches:     103
Percent Similarity: 96.4%    Conservative: 4
Best Local Similarity: 92.8% Mismatches:    4
Query Match:    94.0%       Indels:      0
Db:              9          Gaps:         0

US-10-092-640-36 (1-111) x US-10-679-032-36 (1-333)
QY      1 GlnSerValIleuThrGlnProSerValSerAlaIleProGlyGlnIleValThrIle 20
      |||
Db      1 CAGTCTGTGTTACCGACGCGCCCTCAGTGTCTGCGGCCCGACAGAGTCAACATC 60
QY      21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnIleValSerTrpIleGlnIleu 40
      |||
Db      61 TCCTGCTCTCGAAGCAGCTCCAACTGGGAAATTAATGATCTCGTACACGACGCTC 120
QY      41 ProGlyThrAlaProIleuIleuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
      |||
Db      121 CCAGAAAGGCCCCCAACTCCTCATGTATGATGATCAACCAATCGGCCCTCAGGGTCCCT 180
QY      61 AspArgPheSerGlySerIleSerGlyThrSerAlaSerIleAlaIleSerGlyPheArg 80
      |||
Db      181 GACCGATTCTCTGGCTCCAGTCTGGACCTCAAGCTCCCTGGCATTCAGTGGCTCCGG 240
QY      81 SerGluAspGluAlaAspTyrTrpCysAlaAlaIlePaspAspSerIleuSerGlyTrpVal 100
      |||
Db      241 TCCGAGGATGAGGCTGATTAATGCTGCTCCTGGGACTACACCTGAGTGGTTGGGTG 300
QY      101 PheGlyGlyGlyThrIleuThrValIleuGly 111
      |||
Db      301 TTCCGGGAGGAGCAACAGCTGACCGTCTTAGGT 333

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RESULT 8
US-10-679-032-6
; Sequence 6, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; TITLE OF INVENTION: TREATMENT OF ATHEROSCLEROSIS
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence

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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-679-032-6

Alignment Scores:
Pred. No.: 9,18e-60 Length: 333
Score: 545.00 Matches: 102
Percent Similarity: 95.5% Conservative: 4
Best Local Similarity: 91.9% Mismatches: 5
Query Match: 92.7% Indels: 0
DB: 9 Gaps: 0

US-10-092-640-36 (1-111) x US-10-679-032-6 (1-333)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
DB 1 CAGTCTGTCTGTGCTCAGCCACCCCTCAGGCTTGGAACCCCGGAGAGGGTCAACATC 60
QY 21 SerCysSerGlySerSerSerAenIleGlyAsnAsnTyValSerTrpTyGlnGlnLeu 40
DB 61 TCTTGTCTGGAGAGCTCCATATCGAAGTAATATGTATCTCGTATCAGCAGCTC 120
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgLysIleThrAsnArgProAlaGlyValPro 60
DB 121 CAGGAAACGGCCCCCAAACTCTCATCTATGTGTAACATCAATCGGCCCTCAGGGGTCCCT 180
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCCG 240
QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaTrpAspAspSerLeuSerGlyTrpVal 100
DB 241 TCCGAGATGAGGCTGATTAATTACTGTGACGATGAGATGACACCGCTGAGTGGTG 300
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
DB 301 TTCGGCGAGAGAACCAAGCTGACGGTCTTAGGT 333

RESULT 9
US-10-679-032-30
; Sequence 30, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; TITLE OF INVENTION: TREATMENT OF ATHEROSCLEROSIS
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 30
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-679-032-30

Alignment Scores:
Pred. No.: 1,3e-58 Length: 333
Score: 536.00 Matches: 100
Percent Similarity: 94.6% Conservative: 5
Best Local Similarity: 90.1% Mismatches: 6
Query Match: 91.2% Indels: 0
DB: 9 Gaps: 0

US-10-092-640-36 (1-111) x US-10-679-032-30 (1-333)

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QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
DB 1 CAGTCTGTCTGTGCTCAGCCACCCCTCAGGCTTGGAACCCCGGAGAGGGTCAACATC 60
QY 21 SerCysSerGlySerSerSerAenIleGlyAsnAsnTyValSerTrpTyGlnGlnLeu 40
DB 61 TCTTGTCTGGAGAGCTCCATATCGAAGTAATATGTATCTCGTATCAGCAGCTC 120
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgLysIleThrAsnArgProAlaGlyValPro 60
DB 121 CAGGAAACGGCCCCCAAACTCTCATCTATGTGTAACATCAATCGGCCCTCAGGGGTCCCT 180
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCCG 240
QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaTrpAspAspSerLeuSerGlyTrpVal 100
DB 241 TCCGAGATGAGGCTGATTAATTACTGTGACGATGAGATGACACCGCTGAGTGGTG 300
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
DB 301 TTCGGCGAGAGAACCAAGCTGACGGTCTTAGGT 333

RESULT 10
US-10-679-032-2
; Sequence 2, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; TITLE OF INVENTION: TREATMENT OF ATHEROSCLEROSIS
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-679-032-2

Alignment Scores:
Pred. No.: 2,75e-58 Length: 336
Score: 533.50 Matches: 101
Percent Similarity: 93.8% Conservative: 4
Best Local Similarity: 90.2% Mismatches: 6
Query Match: 90.7% Indels: 1
DB: 9 Gaps: 1

US-10-092-640-36 (1-111) x US-10-679-032-2 (1-336)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
DB 1 CAGTCTGTCTGTGCTCAGCCACCCCTCAGGCTTGGAACCCCGGAGAGGGTCAACATC 60
QY 21 SerCysSerGlySerSerSerAenIleGlyAsnAsnTyValSerTrpTyGlnGlnLeu 40
DB 61 TCTTGTCTGGAGAGCTCCATATCGAAGTAATATGTATCTCGTATCAGCAGCTC 120
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgLysIleThrAsnArgProAlaGlyValPro 60
DB 121 CAGGAAACGGCCCCCAAACTCTCATCTATGTGTAACATCAATCGGCCCTCAGGGGTCCCT 180
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80

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Db      181 GACCATTCCTCGGCTCCAAAGTCTGGCACTCAGCTCCCTCCCTCAGTGGGCTCCGG 240
Qy      81 SerGluaspGluAlaAspTyrTyrCysAlaAlaATPPaspSerLeuSerGly---Tyr 99
Db      241 TCCGAGGATGAGGCTGATTAATTACTGTGAGCATGGATGACAGCTGAATGTCATTGG 300
Qy      100 ValPheGlyGlyThrTyrLeuThrValLeuGly 111
Db      301 GTGTTGGGGAGGAAACAAGCTGACGGTCTTAGGT 336

RESULT 11
US-10-679-032-34
; Sequence 34, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 34
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-34

Alignment Scores:
Pred. No.:      5,686-58      Length:      333
Score:          531.00      Matches:      99
Percent Similarity: 93.7%      Conservative: 5
Best Local Similarity: 89.2%      Mismatches: 7
Query Match:    90.3%      Indels:      0
DB:             9          Gaps:          0

US-10-092-640-36 (1-111) x US-10-679-032-34 (1-333)
Qy      1 GlnSerValLeuThrGlnProSerValSerAlaAlaProGlyGlnLysValThrIle 20
Db      1 CAGTCTGTCTGACTCAGCCACCTCAGGGCTCGGAGCCCGGAGAGGGTCAACATC 60
Qy      21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
Db      61 TCCCTTTTCGAGAGAGAGCTCCAAACATCGGAATTAATGTGTAACAGCTGATCAGAGCTC 120
Qy      41 ProGlyThrAlaProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
Db      121 CCAGAGACGGCCCCCAAACTCCTCATCTATGTGTAACAACAATCGGCCCCCTCAGGGGCTCCCT 180
Qy      61 AspArgPheSerSerGlySerLeuSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db      181 GACCATTCCTCGGCTCCAAAGTCTGGCACTCAGCTCCCTGGCCATCAGTGGGCTCCGG 240
Qy      81 SerGluaspGluAlaAspTyrTyrCysAlaAlaATPPaspSerLeuSerGlyTyrPVal 100
Db      241 TCCGAGGATGAGGCTGATTAATTACTGTGAGCATGGATGACAGCTGCGTGGTGGCTG 300
Qy      101 PheGlyGlyGlyThrTyrLeuThrValLeuGly 111
Db      301 TTCGGCGAGGAAACAAGCTGACGGTCTTAGGT 333

RESULT 12
US-10-679-032-8
; Sequence 8, Application US/10679032
```

```
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-8

Alignment Scores:
Pred. No.:      1,026-57      Length:      333
Score:          529.00      Matches:      99
Percent Similarity: 92.8%      Conservative: 4
Best Local Similarity: 89.2%      Mismatches: 8
Query Match:    90.0%      Indels:      0
DB:             9          Gaps:          0

US-10-092-640-36 (1-111) x US-10-679-032-8 (1-333)
Qy      1 GlnSerValLeuThrGlnProSerValSerAlaAlaProGlyGlnLysValThrIle 20
Db      1 CAGTCTGTCTGACTCAGCCACCTCAGGGCTCGGAGCCCGGAGAGGGTCAACATC 60
Qy      21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
Db      61 TCCCTCTCTGAGAGAGCTCCAACTTGGAAATTAATCTATGTTCTGTGATAGAGAGCTC 120
Qy      41 ProGlyThrAlaProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
Db      121 CCAGAGACGGCCCCCAAACTCCTCATCTATGTAATAATCAAGCGGCCCCCTCAGGGGCTCCCT 180
Qy      61 AspArgPheSerSerGlySerLeuSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db      181 GACCATTCCTCGGCTCCAAAGTCTGGCACTCAGCTCCCTGGCCATCAGTGGGCTCCGG 240
Qy      81 SerGluaspGluAlaAspTyrTyrCysAlaAlaATPPaspSerLeuSerGlyTyrPVal 100
Db      241 TCCGAGGATGAGGCTGATTAATTACTGTGAGCATGGATGACAGCTGAGTCAATTGGCTG 300
Qy      101 PheGlyGlyGlyThrTyrLeuThrValLeuGly 111
Db      301 TTCGGCGAGGAAACAAGCTGACGGTCTTAGGT 333

RESULT 13
US-10-679-032-38
; Sequence 38, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 38
```

```

/ LENGTH: 333
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-38

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Alignment Scores:
Pred. No.: 1.84e-57 Length: 333
Score: 527.00 Matches: 98
Percent Similarity: 93.7% Conservative: 6
Best Local Similarity: 88.3% Mismatches: 7
Query Match: 89.6% Indels: 0
DB: 9 Gaps: 0

```

US-10-092-640-36 (1-111) x US-10-679-032-38 (1-333)

```

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
    |||||
DB 1 CAGTCTGTGCTGACTGACCCACCTCAGCCTCTGGGACCCCGGAGGAGGTCCACCATC 60
    |||||
QY 21 SerCysSerGlySerSerSerSerAenIleGlyAsnAsnTyValSerTrpTyrgInGlnLeu 40
    |||||
DB 61 TCCTGCTCTGGAGACAGCTCCAGCATTTGGGAATTAATTATCTCTGTTATCAGCAGCTC 120
    |||||
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgLysHisThrAsnArgProAlaGlyValPro 60
    |||||
DB 121 CCAGGAACGGCCCCCAAACTCTCATCTATGACAAATATGAAGGAGACCTCAGGGGTCCTT 180
    |||||
QY 61 AspArgPheSerGlySerGlySerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
    |||||
DB 181 GACCGATTCTCTGGCTCCAGTCTGGACCTTGACCTCCTGCGCATCAGTGGGCTCCGG 240
    |||||
QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaATPAspAspSerLeuSerGlyTrpVal 100
    |||||
DB 241 TCCGAGATGAGGCTGATTATTAATCTGTGCAAGCATGGGATACAGCTGAATGGTTGGGTG 300
    |||||
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
    |||||
DB 301 TTCGGCGGAGGAACCAAGCTGACGGTCTTAGGT 333
    |||||

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RESULT 14

```

US-10-679-032-10
/ Sequence 10, Application US/10679032
/ Publication No. US20040202653A1
/ GENERAL INFORMATION:
/ APPLICANT: NILSSON, JAN
/ APPLICANT: CARLSSON, ROLAND
/ APPLICANT: BENGTSSON, JENNY
/ APPLICANT: STRANDBERG, LEIF
/ TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
/ FILE REFERENCE: 7303CIP
/ CURRENT APPLICATION NUMBER: US/10/679,032
/ NUMBER OF SEQ ID NOS: 79
/ SOFTWARE: Patentin Ver. 3.2
/ SEQ ID NO 10
/ LENGTH: 333
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-10

```

```

Alignment Scores:
Pred. No.: 3.32e-57 Length: 333
Score: 525.00 Matches: 98
Percent Similarity: 91.9% Conservative: 4
Best Local Similarity: 88.3% Mismatches: 9
Query Match: 89.3% Indels: 0

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DB: 9 Gaps: 0

US-10-092-640-36 (1-111) x US-10-679-032-10 (1-333)

```

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
    |||||
DB 1 CAGTCTGTGCTGACTGACCCACCTCAGCCTCTGGGACCCCGGAGGAGGTCCACCATC 60
    |||||
QY 21 SerCysSerGlySerSerSerSerAenIleGlyAsnAsnTyValSerTrpTyrgInGlnLeu 40
    |||||
DB 61 TCCTGCTCTGGAGACAGCTCCAGCATTTGGGAATTAATTATCTCTGTTATCAGCAGCTC 120
    |||||
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgLysHisThrAsnArgProAlaGlyValPro 60
    |||||
DB 121 CCAGGAACGGCCCCCAAACTCTCATCTATGAGAAATATGAGGAGGAGGTCCTT 180
    |||||
QY 61 AspArgPheSerGlySerGlySerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
    |||||
DB 181 GACCGATTCTCTGGCTCCAGTCTGGACCTTGACCTCCTGCGCATCAGTGGGCTCCGG 240
    |||||
QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaATPAspAspSerLeuSerGlyTrpVal 100
    |||||
DB 241 TCCGAGATGAGGCTGATTATTAATCTGTGCAAGCATGGGATGACAGCTGAATGGTTGGGTG 300
    |||||
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
    |||||
DB 301 TTCGGCGGAGGAACCAAGCTGACGGTCTTAGGT 333
    |||||

```

RESULT 15

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US-10-679-032-20
/ Sequence 20, Application US/10679032
/ Publication No. US20040202653A1
/ GENERAL INFORMATION:
/ APPLICANT: NILSSON, JAN
/ APPLICANT: CARLSSON, ROLAND
/ APPLICANT: BENGTSSON, JENNY
/ APPLICANT: STRANDBERG, LEIF
/ TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
/ FILE REFERENCE: 7303CIP
/ CURRENT APPLICATION NUMBER: US/10/679,032
/ NUMBER OF SEQ ID NOS: 79
/ SOFTWARE: Patentin Ver. 3.2
/ SEQ ID NO 20
/ LENGTH: 336
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-20

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Alignment Scores:
Pred. No.: 3.9e-57 Length: 336
Score: 524.50 Matches: 100
Percent Similarity: 92.9% Conservative: 4
Best Local Similarity: 89.3% Mismatches: 7
Query Match: 89.2% Indels: 1
DB: 9 Gaps: 1

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US-10-092-640-36 (1-111) x US-10-679-032-20 (1-336)

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QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
    |||||
DB 1 CAGTCTGTGCTGACTGACCCACCTCAGCCTCTGGGACCCCGGAGGAGGTCCACCATC 60
    |||||
QY 21 SerCysSerGlySerSerSerSerAenIleGlyAsnAsnTyValSerTrpTyrgInGlnLeu 40
    |||||
DB 61 TCCTGCTCTGGAGACAGCTCCAGCATTTGGGAATTAATTATCTCTGTTATCAGCAGCTC 120
    |||||
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgLysHisThrAsnArgProAlaGlyValPro 60
    |||||

```

```

Db      121 CCAGGACGGCCCCCAACTCCTCATCTATAGGAATATCAGGGCCCTCAGGGGTCCCT 180
QY      61 AspaGPhneSerGlySerIySerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db      181 GACCGATTCTCTGGCTCCAAAGTGTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
QY      81 SerGIuAspGIuAlaAspTYrTYrCysAlaAlaTrpAspAspSerLeuSerGly---Trp 99
Db      241 TCCGAGGATGAGGCTGATTATTACTGTGCAAGCATGGGATGACAGCCTGAAATGTCATTGG 300
QY      100 ValPheGlyGlyGlyThrIySLeuThrValIleuGly 111
Db      301 GTGTTGGGGGAGGAACCAAGCTGACGGTCTTAGGT 336

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Search completed: May 25, 2006, 21:27:49
 Job time : 1011.71 secs

us-10-092-640-36.rnpbm

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 20:51:32 ; Search time 17.575 Seconds
(without alignments)
1069.431 Million cell updates/sec

Title: US-10-092-640-36
Perfect score: 588
Sequence: 1 QSVLTQPPVSAAPGQKVTI.....WDSLSGWFVGGTKLTVLG 111

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abs/ABSSMBE.spool/US10092640/runat_25052006_155730_6141/app.query.fasta_1
-DB=Published Applications NA New -OPMT=fastcap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-PPANS=human0.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abss62h
-USER=US10092640 @CGN 1.1.26 @runat_25052006_155730_6141 -NCPU=6 -ICPU=3
-NO MAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=10
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505.5	86.0	764	6	US-10-503-433B-11 Sequence 11, Appl
2	497.5	84.6	732	6	US-10-503-433B-16 Sequence 16, Appl
3	497.5	84.6	795	6	US-10-503-433B-12 Sequence 12, Appl
4	493.5	83.9	873	7	US-11-154-103-27 Sequence 27, Appl
5	493.5	83.9	873	7	US-11-154-103-28 Sequence 28, Appl
6	490.5	82.4	801	6	US-10-503-433B-14 Sequence 14, Appl
7	484.5	82.4	796	6	US-10-503-433B-24 Sequence 24, Appl
8	466.5	79.3	803	6	US-10-503-433B-20 Sequence 20, Appl
9	456.5	77.6	792	6	US-10-503-433B-21 Sequence 21, Appl

10	454.5	77.3	779	6	US-10-503-433B-18	Sequence 18, Appl
11	452	76.9	333	7	US-11-254-679-31	Sequence 31, Appl
12	451.5	76.8	722	6	US-10-503-433B-22	Sequence 22, Appl
13	444.5	75.6	706	6	US-10-503-433B-17	Sequence 17, Appl
14	436.5	73.8	704	6	US-10-503-433B-15	Sequence 15, Appl
15	434	73.4	864	7	US-11-154-103-29	Sequence 29, Appl
16	431.5	73.4	330	7	US-11-254-679-63	Sequence 63, Appl
17	424.5	72.2	707	6	US-10-503-433B-19	Sequence 19, Appl
18	420	71.4	1954	7	US-11-293-697-1648	Sequence 1648, Ap
19	412	70.1	1912	7	US-11-293-697-1818	Sequence 1818, Ap
20	409	69.6	885	7	US-11-154-103-33	Sequence 33, Appl
21	399	67.9	330	6	US-10-499-266-13	Sequence 13, Appl
22	392	66.7	729	7	US-11-154-103-20	Sequence 20, Appl
23	385.5	65.6	870	7	US-11-154-103-30	Sequence 30, Appl
24	356	60.5	873	7	US-11-154-103-32	Sequence 32, Appl
25	335.5	57.1	637	6	US-10-503-433B-23	Sequence 23, Appl
26	334	56.8	2081	7	US-11-293-697-2348	Sequence 2348, Ap
27	333	56.6	330	7	US-11-300-563-24	Sequence 24, Appl
28	332	56.5	543	7	US-11-301-554-970	Sequence 970, Appl
29	317	53.9	4027	7	US-11-169-140-1	Sequence 1, Appl
30	298	50.7	608	7	US-11-301-554-908	Sequence 908, Appl
31	284	48.3	726	7	US-11-183-325-19	Sequence 19, Appl
32	276.5	47.0	592	6	US-10-503-433B-13	Sequence 13, Appl
33	268	45.6	330	7	US-11-254-679-35	Sequence 35, Appl
34	268	45.6	384	7	US-11-183-218-59	Sequence 59, Appl
35	268	45.6	9209	7	US-11-183-218-58	Sequence 58, Appl
36	267.5	45.5	321	7	US-11-219-563-52	Sequence 52, Appl
37	264.5	45.0	322	7	US-11-211-917-83	Sequence 83, Appl
38	264.5	45.0	705	7	US-11-211-917-87	Sequence 87, Appl
39	262	44.6	333	7	US-11-216-033-11	Sequence 11, Appl
40	261	44.4	384	7	US-11-315-067-3	Sequence 3, Appl
41	261	44.4	384	7	US-11-315-067-5	Sequence 5, Appl
42	260.5	44.3	620	7	US-11-219-563-56	Sequence 56, Appl
43	260.5	44.3	620	7	US-11-219-563-58	Sequence 58, Appl
44	260.5	44.3	2196	7	US-11-155-444-5	Sequence 5, Appl
45	260.5	44.3	2208	7	US-11-155-444-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-10-503-433B-11
; Sequence 11, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 11
; LENGTH: 764
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P8 Scfv binding site (template DNA)
US-10-503-433B-11

Alignment Scores:
Pred. No.: 1.53e-47
Score: 505.50
Percent Similarity: 91.1%
Best Local Similarity: 87.5%
Query Match: 86.0%
DB: 6
Gaps: 1
Length: 764
Matches: 98
Conservative: 4
Mismatch: 9
Indels: 1

US-10-092-640-36 (1-111) x US-10-503-433B-11 (1-764)

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QY      1 GlnSerValLeuThrGlnProSerValSerAlaAlaProGlyGlnIleValThrIle 20
Db      397 CAGTCTGTCGACTGACCGACCTCAGCGCTCGGAGACCCCGGGGAGAGGGGTACACATC 456
QY      21 SerCySerGlySerSerSerSerAsnIleGlyAsnAsnTyr---ValSerTyrPylGlnGln 39
Db      457 TCTTGCACTGGGAGAGAGCTCCAACATCGGGGAGGTTAGATGATACCTGGTATCAGCAG 516
QY      40 LeuProGlyThrAlaProIleLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
Db      517 CTCGAGGAGAACGGCCCCCAACTCCTCATCTATGTGTAACAACATCGGCCCTCAGGGGCTC 576
QY      60 ProAspArgPheSerGlySerIleSerGlyThrSerAlaSerIleuAlaIleSerGlyPhe 79
Db      577 CCTGACCGAATTCCTGGCTCCAAAGTCTGGCACTCGCTCCCTGGCCATCAGTGGGCTC 636
QY      80 ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaIleTrpAspSerLeuSerGlyTyr 99
Db      637 CGGTCCGAGATGAGAGGCTGATTATTAATCTGTGGCGCTTGGAATGACAGCTGAGTGGTCA 696
QY      100 ValPheGlyGlyGlyThrIleLeuThrValLeuGly 111
Db      697 GTGTTCCGGCGAGGAACCAAGCTGACGCTCCTAGGT 732

RESULT 2
US-10-503-433B-16
; Sequence 16, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT FILING DATE: 2004-08-02
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqMan9
; SEQ ID NO 16
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 1-13
US-10-503-433B-16

Alignment Scores:
Pred. No.: 1,11e-46      Length: 732
Score: 497.50           Matches: 96
Percent Similarity: 89.3%      Conservative: 4
Best Local Similarity: 85.7%   Mismatches: 11
Query Match: 84.6%         Indels: 1
DB: 6                   Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-16 (1-732)
QY      1 GlnSerValLeuThrGlnProSerValSerAlaAlaProGlyGlnIleValThrIle 20
Db      397 CAGTCTGTCGACTGACCGACCTCAGCGCTCGGAGACCCCGGGGAGAGGGGTACACATC 456
QY      21 SerCySerGlySerSerSerSerAsnIleGlyAsnAsnTyr---ValSerTyrPylGlnGln 39
Db      457 TCTTGCACTGGGAGAGAGCTCCAACATCGGGGAGGTTAGATGATACCTGGTATCAGCAG 516
QY      40 LeuProGlyThrAlaProIleLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
Db      517 CTCGAGGAGAACGGCCCCCAACTCCTCATCTATGTGTAACAACATCGGCCCTCAGGGGCTC 576
QY      60 ProAspArgPheSerGlySerIleSerGlyThrSerAlaSerIleuAlaIleSerGlyPhe 79
Db      577 GTGTTCCGGCGAGGAACCAAGCTGACGCTCCTAGGT 732
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Db      577 CCTGACCGAATTCCTGGCTCCAAAGTCTGGCACTCAGCGCTCCCTGGCCATCAGTGGGCTC 636
QY      80 ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaIleTrpAspSerLeuSerGlyTyr 99
Db      637 CGGTCCGAGATGAGAGGCTGATTATTAATCTGTGGCGCTTGGAATGACAGCTCGTGGTACG 696
QY      100 ValPheGlyGlyGlyThrIleLeuThrValLeuGly 111
Db      697 GTGTTCCGGCGAGGAACCAAGCTGACGCTCCTAGGT 732

RESULT 3
US-10-503-433B-12
; Sequence 12, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT FILING DATE: 2004-08-02
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqMan9
; SEQ ID NO 12
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 1-1
US-10-503-433B-12

Alignment Scores:
Pred. No.: 1,24e-46      Length: 795
Score: 497.50           Matches: 96
Percent Similarity: 91.1%      Conservative: 6
Best Local Similarity: 85.7%   Mismatches: 9
Query Match: 84.6%         Indels: 1
DB: 6                   Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-12 (1-795)
QY      1 GlnSerValLeuThrGlnProSerValSerAlaAlaProGlyGlnIleValThrIle 20
Db      396 CAGTCTGTCGACTGACCGACCTCAGCGCTCGGAGACCCCGGGGAGAGGGGTACACATC 455
QY      21 SerCySerGlySerSerSerSerAsnIleGlyAsnAsnTyr---ValSerTyrPylGlnGln 39
Db      456 TCTTGCACTGGGAGAGAGCTCCAACATCGGGGAGGTTAGATGATACCTGGTATCAGCAG 515
QY      40 LeuProGlyThrAlaProIleLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
Db      516 CTCGAGGAGAACGGCCCCCAACTCCTCATCTATGTGTAACAACATCGGCCCTCAGGGGCTC 575
QY      60 ProAspArgPheSerGlySerIleSerGlyThrSerAlaSerIleuAlaIleSerGlyPhe 79
Db      576 CCTGACCGAATTCCTGGCTCCAAAGTCTGGCACTCAGCGCTCCCTGGCCATCAGTGGGCTC 635
QY      80 ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaIleTrpAspSerLeuSerGlyTyr 99
Db      636 CGGTCCGAGATGAGAGGCTGATTATTAATCTGTGGCGCTTGGAATGACACCTCAGCGGCTCAG 695
QY      100 ValPheGlyGlyGlyThrIleLeuThrValLeuGly 111
Db      696 GTGTTCCGGCGAGGAACCAAGCTGACGCTCCTAGGT 731

RESULT 4
US-11-154-103-27
; Sequence 27, Application US/11154103
; Publication No. US20060099205A1
; GENERAL INFORMATION:
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; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding single chain antibody.
;
US-11-154-103-27

Alignment Scores:
Pred. No.: 3,86e-46 Length: 873
Score: 493.50 Matches: 94
Percent Similarity: 92.0% Conservative: 9
Best Local Similarity: 83.9% Mismatches: 8
Query Match: 83.9% Indels: 1
DB: 7 Gaps: 1

US-10-092-640-36 (1-111) x US-11-154-103-27 (1-873)

QY 1 GlnSerValIleuThrGlnProPseValSerAlaAlaProGlyGlnIysValThrIle 20
DB 469 CAGTCTGTGTAGCGAGCGCCCTCAGTGTCTGGGGCCCCAGGAGAGGTCACCATC 528
QY 21 SerCySerGlySerSerSerSerAnIleGlyAsnAsnTyr--ValSerTyrGlnGln 39
DB 529 TCCTGACACGGAGAGCGCTCAACATCGGGGAGGTATGCTGATACCTGTACCTGCAGCAG 588
QY 40 LeuProGlyThrAlaProIysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
DB 589 CTTCCAGAGAACGCCCCCAACTCTCATCTATGTAACACCATCGGCCCTCAGGGGTC 648
QY 60 ProAspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
DB 649 CCTGACCGATTCTCTGGCTTCAAGTCTGCACCTCAGCTCCTGGCCATCAGTGGGCTC 708
QY 80 ArgSerGluAspGluAlaAspTyrTyrCyAlaAlaIleTTPAspAspSerLeuSerGlyTyr 99
DB 709 CAGCGTGAAGATGAGGCTATTATTAATCTCCAGTCTCTATGACAGCAGCTGAGTGGTGG 768
QY 100 ValPheGlyGlyGlyThrIysLeuThrValLeuGly 111
DB 769 GTGTTGGCGGAGGAGCAAGCTGACCTGACTAAGT 804

RESULT 5
US-11-154-103-28
; Sequence 28, Application US/11154103
; Publication No. US20060099205A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
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; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding single chain antibody.
;
US-11-154-103-28

Alignment Scores:
Pred. No.: 3,86e-46 Length: 873
Score: 493.50 Matches: 94
Percent Similarity: 92.0% Conservative: 9
Best Local Similarity: 83.9% Mismatches: 8
Query Match: 83.9% Indels: 1
DB: 7 Gaps: 1

US-10-092-640-36 (1-111) x US-11-154-103-28 (1-873)

QY 1 GlnSerValIleuThrGlnProPseValSerAlaAlaProGlyGlnIysValThrIle 20
DB 469 CAGTCTGTGTAGCGAGCGCCCTCAGTGTCTGGGGCCCCAGGAGAGGTCACCATC 528
QY 21 SerCySerGlySerSerSerSerAnIleGlyAsnAsnTyr--ValSerTyrGlnGln 39
DB 529 TCCTGACACGGAGAGCGCTCAACATCGGGGAGGTATGCTGATACCTGTACCTGCAGCAG 588
QY 40 LeuProGlyThrAlaProIysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
DB 589 CTTCCAGAGAACGCCCCCAACTCTCATCTATGTAACACCATCGGCCCTCAGGGGTC 648
QY 60 ProAspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
DB 649 CCTGACCGATTCTCTGGCTTCAAGTCTGCACCTCAGCTCCTGGCCATCAGTGGGCTC 708
QY 80 ArgSerGluAspGluAlaAspTyrTyrCyAlaAlaIleTTPAspAspSerLeuSerGlyTyr 99
DB 709 CAGCGTGAAGATGAGGCTATTATTAATCTCCAGTCTCTATGACAGCAGCTGAGTGGTGG 768
QY 100 ValPheGlyGlyGlyThrIysLeuThrValLeuGly 111
DB 769 GTGTTGGCGGAGGAGCAAGCTGACCTGACTAAGT 804

RESULT 6
US-10-503-433B-14
; Sequence 14, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqMan99
; SEQ ID NO 14
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 1-9
;
US-10-503-433B-14

Alignment Scores:
Pred. No.: 7,41e-46 Length: 801
Score: 490.50 Matches: 96
```

Percent Similarity: 90.2% Conservative: 5
Best Local Similarity: 85.7% Mismatches: 10
Query Match: 83.4% Indels: 1
DB: 6 Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-14 (1-801)

```
OY 1 GlnSerValIleuThrGlnProSerValSerAlaAlaProGlyGlnIlyValThrIle 20
DB 397 CAGTCTGTGCTACTCAGCCACCTCAGGCTCTGGAGACCCCGGAGAGGGTCAACATC 456
OY 21 SerCySerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 39
DB 457 TCTTCACACTGGAGAGAGCTCCCAACATCGGGGAGGTAGATGATACATCGATATCAGCAG 516
OY 40 LeuProGlyThrAlaProIlySerLeuLeuIleTyGlyHisThrAsnArgProAlaGlyVal 59
DB 517 CTCCAGAGAACGGCCCCCAACTCCCTCATCTATGTGTACAAACATCGGCCCTCAGGGGCTC 576
OY 60 ProAspArgPheSerGlySerIlySerSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
DB 577 CTTGACCAATCTCTGGCTCCAAAGTCTGGACCTCCTCCCTGACCTCATCGTGGGCTC 636
OY 80 ArgSerGluAspGluAlaAspTyTyTyCysAlaAlaIleTrpAspAspSerLeuSerGlyTrp 99
DB 637 CGGTCCGAGAGATGAGGCTGATTATTAATCTGTGCGGCTCATGATGACAGTATCAGCGGTG 696
OY 100 ValPheGlyGlyGlyThrIlySerLeuThrValLeuGly 111
DB 697 GTGTTCCGGCGAGAACCAAGCTGACGGTCTTAGGT 732
```

RESULT 7

US-10-503-433B-24

```
; Sequence 24, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 24
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-18
US-10-503-433B-24
```

Alignment Scores:

Pred. No.:	3,39e-45	Length:	796
Score:	484.50	Matches:	94
Percent Similarity:	90.2%	Conservative:	7
Best Local Similarity:	83.9%	Mismatches:	10
Query Match:	82.4%	Indels:	1
DB:	6	Gaps:	1

US-10-092-640-36 (1-111) x US-10-503-433B-24 (1-796)

```
OY 1 GlnSerValIleuThrGlnProSerValSerAlaAlaProGlyGlnIlyValThrIle 20
DB 397 CAGTCTGTGCTACTCAGCCACCTCAGGCTCTGGAGACCCCGGAGAGGGTCAACATC 456
OY 21 SerCySerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 39
DB 457 TCTTCACACTGGAGAGCTCCCAACATCGGGGAGGTAGATGATACATCGATATCAGCAG 516
```

```
OY 40 LeuProGlyThrAlaProIlySerLeuLeuIleTyGlyHisThrAsnArgProAlaGlyVal 59
DB 517 CTCCAGAGAACGGCCCCCAACTCCCTCATCTATGTGTACAAACATCGGCCCTCAGGGGCTC 576
OY 60 ProAspArgPheSerGlySerIlySerSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
DB 577 CTTGACCAATCTCTGGCTCCAAAGTCTGGACCTCCTCCCTGACCTCATCGTGGGCTC 636
OY 80 ArgSerGluAspGluAlaAspTyTyTyCysAlaAlaIleTrpAspAspSerLeuSerGlyTrp 99
DB 637 CGGTCCGAGAGATGAGGCTGATTATTAATCTGTGCGGCTCATGATGACATCTCGGTATG 696
OY 100 ValPheGlyGlyGlyThrIlySerLeuThrValLeuGly 111
DB 697 GTGTTCCGGCGAGAACCAAGCTGACGGTCTTAGGT 732
```

RESULT 8

US-10-503-433B-20

```
; Sequence 20, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 20
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-12
US-10-503-433B-20
```

Pred. No.:	3,35e-43	Length:	803
Score:	466.50 <td>Matches:</td> <td>94</td>	Matches:	94
Percent Similarity:	88.5% <td>Conservative:</td> <td>6</td>	Conservative:	6
Best Local Similarity:	83.2% <td>Mismatches:</td> <td>11</td>	Mismatches:	11
Query Match:	79.3% <td>Indels:</td> <td>2</td>	Indels:	2
DB:	6 <td>Gaps:</td> <td>1</td>	Gaps:	1

US-10-092-640-36 (1-111) x US-10-503-433B-20 (1-803)

```
OY 1 GlnSerValIleuThrGlnProSerValSerAlaAlaProGlyGlnIlyValThrIle 20
DB 397 CAGTCTGTGCTACTCAGCCACCTCAGGCTCTGGAGACCCCGGAGAGGGTCAACATC 456
OY 21 SerCySerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 39
DB 457 TCTTCACACTGGAGAGAGCTCCCAACATCGGGGAGGTATTGATGATTAATCGATATCAGCAG 516
OY 40 LeuProGlyThrAlaProIlySerLeuLeuIleTyGlyHisThrAsnArgProAlaGlyVal 59
DB 517 CTCCAGAGAACGGCCCCCAACTCCCTCATCTATGTGTACAAACATCGGCCCTCAGGGGCTC 576
OY 60 ProAspArgPheSerGlySerIlySerSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
DB 577 CTTGACCAATCTCTGGCTCCAAAGTCTGGACCTCCTCCCTGACCTCATCGTGGGCTC 636
OY 80 ArgSerGluAspGluAlaAspTyTyTyCysAlaAlaIleTrpAspAspSerLeuSerGlyTrp 99
DB 637 CGGTCCGAGAGATGAGGCTGATTATTAATCTGTGCGGCTCATGATGACATCTCATAGGGGTG 696
OY 99 ValPheGlyGlyGlyThrIlySerLeuThrValLeuGly 111
DB 697 GTGTTCCGGCGAGAACCAAGCTGACGGTCTTAGGT 733
```

```
RESULT 9
US-10-503-433B-21
; Sequence 21, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 21
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-15
US-10-503-433B-21

Alignment Scores:
Pred. No.: 4,2e-42 Length: 792
Score: 456.50 Matches: 93
Percent Similarity: 90.2% Conservative: 8
Best Local Similarity: 83.0% Mismatches: 10
Query Match: 77.6% Indels: 2
DB: 6 Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-21 (1-792)
QY 1 GlnSerValLeuThrGlnProPseValSerAlaAlaProGlyGlnLysValThrIle 20
Db 396 CAGTCTGTGCTGACTAGCCACCTCAGCCTCTGGAGACCCCGGAGAGGTCACCATC 455
QY 21 SerCySerGlySerSerSerAenIleGlyAsnAsnTyr--ValSerTPYrGlnGln 39
Db 456 TCTTGACACTGGGAGCAGCTCCAACTCGGGGAGAGTATGATACCTGTTACGAG 515
QY 40 LeuProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
Db 516 CTCCTCCAGAACGGCCCCCAAACTCTCATCTATGTAACAACAATCGGCCCTCAGGGGCTC 575
QY 60 ProAspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
Db 576 CCGTACCGGATTCCTCTGCTCCAGCTCGGACCTCGACCTCCCTGGCCATCAGTGGGCTC 635
QY 80 ArgSerGluAspGluAlaAspTyrTyrCyAsnAlaAlaTrpAspAspSerLeuSerGlyTyr 99
Db 636 CGGTCCGAGAGATGAGGCTGATTTACTGTGCGGCTTTTGATGACACCATTTATGTGCC 695
QY 100 ValPheGlyGlyGlyThrLysLeuThrValLeuGly 111
Db 696 GTGTTCGGCGAGAGAAC-AAAGCTGAGAGGCTCTTAGGT 730

RESULT 10
US-10-503-433B-18
; Sequence 18, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
```

```
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 18
; LENGTH: 779
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-1
US-10-503-433B-18

Alignment Scores:
Pred. No.: 6,84e-42 Length: 779
Score: 454.50 Matches: 94
Percent Similarity: 88.4% Conservative: 5
Best Local Similarity: 83.9% Mismatches: 12
Query Match: 77.3% Indels: 2
DB: 6 Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-18 (1-779)
QY 1 GlnSerValLeuThrGlnProPseValSerAlaAlaProGlyGlnLysValThrIle 20
Db 397 CAGTCTGTGCTGACTAGCCACCTCAGCCTCTGGAGACCCCGGAGAGGTCACCATC 456
QY 21 SerCySerGlySerSerSerAenIleGlyAsnAsnTyr--ValSerTPYrGlnGln 39
Db 457 TCTTGACACTGGGAGCAGCTCCAACTCGGGGAGAGTATGATGATACCTGTTACAGAG 516
QY 40 LeuProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
Db 517 CTCCTCCAGAACGGCCCCCAAACTCTCATCTATGTAACAACAATCGGCCCTCAGGGGCTC 576
QY 60 ProAspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
Db 577 CCGTACCGGATTCCTCTGCTCCAGCTCGGACCTCGACCTCCCTGGCCATCAGTGGGCTC 636
QY 80 ArgSerGluAspGluAlaAspTyrTyrCyAsnAlaAlaTrpAspAspSerLeuSerGlyTyr 99
Db 637 CGGTCCGAGAGATGAGGCTGATTTACTGTGCGGCTTTTGATGACACCATTTATGTGCC 695
QY 100 ValPheGlyGlyGlyThrLysLeuThrValLeuGly 111
Db 696 GTGTTCGGCGAGAGAACCAAGCTGAGAGGCTCTTAGGT 731

RESULT 11
US-11-254-679-31
; Sequence 31, Application US/11254679
; Publication No. US20060099207A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Allan, Christian
; APPLICANT: Gao, Changshou
; APPLICANT: An, Ling-Ling
; APPLICANT: Kiemer, Peter
; APPLICANT: Mao, Su-Yau
; APPLICANT: Coyle, Anthony
; TITLE OF INVENTION: High Affinity Antibodies Against HMB1 and Method of Use Thereof
; FILE REFERENCE: HB601US
; CURRENT APPLICATION NUMBER: US/11/254,679
; PRIOR FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: 60/620,726
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: 60/651,512
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/658,572
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/662,944
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/713,712
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 31
```

```

; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-254-679-31

Alignment Scores:
Pred. No.: 4,28e-42 Length: 333
Score: 452.00 Matches: 88
Percent Similarity: 87.3% Conservative: 8
Best Local Similarity: 80.0% Mismatches: 14
Query Match: 76.9% Indels: 0
DB: 7 Gaps: 0

US-10-092-640-36 (1-111) x US-11-254-679-31 (1-333)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
   |||||
DB 4 CAGAGCGAATTACCTCAGCCCTCGGTGTGAAAGCCCGGCGAGAGGTCAACATC 63

QY 21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTyrValSerTrpTyrGlnGlnLeu 40
   |||||
DB 64 TCTGTCTTCTGGAAGACCTCCAAACATCGAAATTAATGCTGTATCTGTATCCAGAGCTTC 123

QY 41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
   |||||
DB 124 CCAGAAAGGCTCCCAAACCTCCATCTATATGATGATCTGCTGCCCTCAGGGGTCTCT 183

QY 61 AspaArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
   |||||
DB 184 GACCAATTTCTTGGCTCCAAAGTCTGGCACTCAGGCTCCCTGGCCATCAGTGGGCTCCAG 243

QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaATPAspAspSerLeuSerGlyTyrVal 100
   |||||
DB 244 TCTGAGATGAGAGCTGACCTACTTACTGATCATGAGATGAGACCACTGAATGTCGGCTG 303

QY 101 PheGlyGlyGlyThrLysLeuThrValLeu 110
   |||||
DB 304 TTCGGCGAGGAGCAACAGTTGACCGTCTTA 333

RESULT 12
US-10-503-433B-22
; Sequence 22, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqMan99
; SEQ ID NO 22
; LENGTH: 722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-20
US-10-503-433B-22

Alignment Scores:
Pred. No.: 1,33e-41 Length: 722
Score: 451.50 Matches: 91
Percent Similarity: 89.9% Conservative: 7
Best Local Similarity: 83.5% Mismatches: 10
Query Match: 76.8% Indels: 2
DB: 6 Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-22 (1-722)

```

```

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
   |||||
DB 396 CAGTCTGTGCTACTCAGCCACCTCAGCGTGTGGAGACCCCGGCGAGAGGTCAACATC 455

QY 21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTyrValSerTrpTyrGlnGlnLeu 39
   |||||
DB 456 TCTTCACTGGAGAGCAGCTCCAAACATCGGGGAGAGTACGATGTACACTGTATCAGCAG 515

QY 40 LeuProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
   |||||
DB 516 CTCCAGAGAACGCCCCCAAACCTCTCATATGTGTAAACAAATCGGCGCTCAGGGGCTC 575

QY 60 ProAspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
   |||||
DB 576 CCTGACCAATTTCTCGGCTCCAAAGTCTGGCACTCAGCTCCCTGCCATCAGTGGGCTC 635

QY 80 ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaATPAspAspSerLeuSerGlyTyr 99
   |||||
DB 636 CGGTCCGAGATGAGAGCTGATATTAATCTGCGGCTTATGATGACAGATATGATGTCAG 695

QY 100 ValPheGlyGlyGlyThrLysLeuThr 108
   |||||
DB 696 GTTTCGGCGGAGA-ACCAAGCTGACG 721

RESULT 13
US-10-503-433B-17
; Sequence 17, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqMan99
; SEQ ID NO 17
; LENGTH: 706
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 1-20
US-10-503-433B-17

Alignment Scores:
Pred. No.: 7,67e-41 Length: 706
Score: 444.50 Matches: 86
Percent Similarity: 89.3% Conservative: 6
Best Local Similarity: 83.5% Mismatches: 10
Query Match: 75.6% Indels: 1
DB: 6 Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-17 (1-706)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
   |||||
DB 397 CAGTCTGTGCTACTCAGCCACCTCAGCGTGTGGAGACCCCGGCGAGAGGTCAACATC 456

QY 21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTyrValSerTrpTyrGlnGlnLeu 39
   |||||
DB 457 TCTTCACTGGAGAGCAGCTCCAAACATCGGGGAGAGTATGATGTACACTGTATCAGCAG 516

QY 40 LeuProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
   |||||
DB 517 CTCCAGAGAACGCCCCCAAACCTCTCATATGTGTAAACAAATCGGCGCTCAGGGGCTC 576

QY 60 ProAspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
   |||||
DB 577 CCTGACCAATTTCTCGGCTCCAAAGTCTGGCACTCAGCTCCCTGCCATCAGTGGGCTC 636

```

```
QY      80  ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerGlyTrp 99
      |||
Db      637  CGGTCCGAGATAGAGCTGATTATTACTGTGGCTTACATGACGGCCCTAACTGAGT 696
QY      100  ValPheGly 102
      |||
Db      697  GTGTTCCGC 705

RESULT 14
US-10-503-433B-15
; Sequence 15, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 15
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 1-10
US-10-503-433B-15

Alignment Scores:
Pred. No.:      5,86e-40      Length:      704
Score:          436.50      Matches:      84
Percent Similarity: 90.2%      Conservative: 8
Best Local Similarity: 82.4%      Mismatches: 9
Query Match:    74.2%      Indels:      1
DB:             6           Gaps:      1

US-10-092-640-36 (1-111) x US-10-503-433B-15 (1-704)
QY      1  GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
      |||
Db      397  CAGTCTGTGTCGTAGCAGCAGCCCTCAGCGCTGGAGACCCCGGAGAGAGGTCCACCATC 456
QY      21  SerCysSerGlySerSerSerSerAlaIleGlyAsnAsnTyr---ValSerTyrGlnGln 39
      |||
Db      457  TCTTGACACTGGAGAGAGCTCCCAACATCGGGGAGGTTATGATGATATCTGGTATCAGCAG 516
QY      40  LeuProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
      |||
Db      517  CTCCCGAGAACGGCCCCCAACCTCCATCTATGTAACAACAATCGGCCCTCAGAGGGGTC 576
QY      60  ProAspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
      |||
Db      577  CCGTCCGAGATAGAGCTGATTATTACTGTGGCTTACATGACGGCCCTAACTGAGT 636
QY      80  ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerGlyTrp 99
      |||
Db      637  CGGTCCGAGATAGAGCTGATTATTACTGTGGCTTACATGACGGCTTTGATGACGCTATCAGGTTTG 696
QY      100  ValPhe 101
      |||
Db      697  GTGTTCC 702

RESULT 15
US-11-154-103-29
; Sequence 29, Application US/11154103
; Publication No. US20060099205A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
```

```
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-11-154-103-29

Alignment Scores:
Pred. No.:      1.45e-39      Length:      864
Score:          434.00      Matches:      84
Percent Similarity: 86.6%      Conservative: 13
Best Local Similarity: 75.0%      Mismatches: 13
Query Match:    73.8%      Indels:      2
DB:             7           Gaps:      2

US-10-092-640-36 (1-111) x US-11-154-103-29 (1-864)
QY      1  GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
      |||
Db      463  CAGTCTGTGTTGAGCCAGCGCCCTCGTATCTGGGGCCCCCAGGAGAGGTCCACCATC 522
QY      21  SerCysSerGlySerSerSerSerAlaIleGlyAsnAsnTyr---ValSerTyrGlnGln 39
      |||
Db      523  TCCTGCACTGGGAGAGCTCCCAACATCGGGGCAAGTTTGTATGATGATACGTGTACCAAGCAA 582
QY      40  LeuProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
      |||
Db      583  CTTCAGAGAACAGCCCCCAACCTCCATCTATGTAACAACAATCGGCCCTCAGAGGGTC 642
QY      60  ProAspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
      |||
Db      643  CTGACCGAATTCTCTCCCTCCCAAGTCTGGACCTCAGCCCTGGGCACTACCGGACTC 702
QY      80  ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerGlyTrp 99
      |||
Db      703  CAGATCGGGGACCAAGCCGATTATTACTCGGCTCATATACAGCACCTACTCT---TGG 759
QY      100  ValPheGlyGlyThrLysLeuThrValLeuGly 111
      |||
Db      760  GTGTTCCGAGAGAGCAAGGTACCTGCTTAGGT 795

Search completed: May 25, 2006, 21:28:33
Job time : 20.575 secs
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OM protein - nucleic search, using frame_plus_p2n model1

Run on: May 25, 2006, 16:11:24 ; Search time 4911.14 Seconds
(without alignments)
2519.344 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700

Sequence: 1 QVQLQSGAEGLKKGPSLKI.....AKKPEYFGHGGQTVTVSS 129

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 segs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi -LIST=45
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_pat:*
3: gb_ph:*
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10: gb_vi:*
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12: gb_ncg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	700	100.0	387	5	HSU36542	U36542 Human anti-
2	700	100.0	387	5	HSU38328	U38328 Human anti-
3	700	100.0	387	5	HSU38331	U38331 Human anti-

4	700	100.0	387	5	HSU38332	U38332 Human anti-
5	700	100.0	774	2	AR083879	AR083879 Sequence
6	700	100.0	774	2	AR278815	AR278815 Sequence
7	697	99.6	1509	8	AF516873	AF516873 Synthetic
8	694	99.1	387	5	HSU38333	U38333 Human anti-
9	692	98.9	387	5	HSU38330	U38330 Human anti-
10	689	98.4	387	5	HSU38224	U38224 Human anti-
11	688	98.3	387	5	HSU38323	U38323 Human anti-
12	684	97.7	387	5	HSU38329	U38329 Human anti-
13	683	97.6	387	5	HSU38327	U38327 Human anti-
14	683	97.6	387	5	HSU38334	U38334 Human anti-
15	682	97.4	387	5	HSU36543	U36543 Human anti-
16	680	97.1	387	5	HSU38326	U38326 Human anti-
17	669	95.6	387	5	HSU36552	U36552 Human anti-
18	669	95.6	387	5	HSU36557	U36557 Human anti-
19	669	95.6	387	5	HSU38324	U38324 Human anti-
20	666	95.1	387	5	HSU36544	U36544 Human anti-
21	666	95.1	387	5	HSU36547	U36547 Human anti-
22	663	94.7	387	5	HSU36550	U36550 Human anti-
23	663	94.7	387	5	HSU36551	U36551 Human anti-
24	663	94.7	387	5	HSU36554	U36554 Human anti-
25	661	94.4	387	5	HSU36559	U36559 Human anti-
26	659	94.1	387	5	HSU36549	U36549 Human anti-
27	658	94.0	387	5	HSU36556	U36556 Human anti-
28	657	93.9	387	5	HSU36546	U36546 Human anti-
29	656	93.7	387	5	HSU36535	U36535 Human anti-
30	655	93.6	387	5	HSU36548	U36548 Human anti-
31	648	92.6	387	5	HSU38325	U38325 Human anti-
32	646	92.3	387	5	HSU36545	U36545 Human anti-
33	645	92.1	387	5	HSU36553	U36553 Human anti-
34	639	91.3	387	5	HSU36555	U36555 Human anti-
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36	629	89.9	387	2	HSU36558	U36558 Human anti-
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38	540	77.1	364	2	DD186925	DD186925 Method fo
39	540	77.1	906	2	AX111698	AX111698 Sequence
40	539	77.0	498	5	AY393196	AY393196 Homo sapi
41	537	76.7	375	5	AB067159	AB067159 Homo sapi
42	534	76.3	381	5	AF110484	AF110484 Homo sapi
43	531.5	75.9	381	5	AF174110	AF174110 Homo sapi
44	530.5	75.8	367	5	AF174110	AF174110 Homo sapi
45	530.5	75.8	378	5	HSU77538	U77538 Human clone

ALIGNMENTS

RESULT 1
HSU36542
LOCUS Human anti-c-erbB-2 immunoglobulin heavy chain V region mRNA,
DEFINITION partial cds.
ACCESSION U36542
VERSION U36542.1 GI:1145223
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Schier,R., Bye,J., Apell,G., McCall,A., Adams,G.P., Weiner,L.M. and
Marks,U.D.
TITLE Isolation of high affinity monomeric Human anti-c-erbB-2 single
chain Fv using affinity driven selection
JOURNAL J. Mol. Biol. (1995) In press
REFERENCE
AUTHORS Schier,R.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1995) Robert Schier, Anesthesia, University of
California at San Francisco, 1001 Potrero Avenue, San Francisco, CA
94110, USA
FEATURES
source Location/Qualifiers
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ORIGIN

Alignment Scores:

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Pred. No.: 4,77e-76 Length: 387
Score: 700.00 Matches: 129
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0
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US-10-092-640-32 (1-129) x HSU36542 (1-387)

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DB 1 CAGGTGCACACTGTGTGACGTCTGGGGCAGAGTGAACCCGGGAGTCTCTGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTyrIleAlaTrpValArgIleMet 40
    |||||
DB 61 TCTCTGAAGGGTTCTGGATACAGCTTACCAAGTACCTGATCCCTGGGTGGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnLysMetGlyLeuLysTyrProGlyLysSerAspThrLysTyr 60
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DB 121 CCCGGGAAAGCCTGGAGTACATGAGGGCTCATCTATCTGATGACTGACACCAATATC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
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DB 181 AGCCCGTCTCTCCAAAGCCAGGTCACCACTCAGTGCACAGTCCGTCAGCACTGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
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DB 241 TTGCATATGAGCAGTGTGAAGCCCTCGGACAGGCCCTGTATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerAsnCysAlaLysTrpProGlyLysPheGlnHisTrpGly 120
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DB 301 GTGGGATATTGACAGTATGTTCCAACTGCGCAAGTGGCTGAAATACCTTCAGCATTTGGGCG 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
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DB 361 CAGGGCACCCCTGTGACCGTCTCTCA 387
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RESULT 2
LOCUS HSU38328 387 bp mRNA linear PRI 02-OCT-1996
DEFINITION Human anti-c-erbB-2 immunoglobulin heavy chain V mRNA, partial cds,
clone C6PM7.

ACCESSION U38328
VERSION U38328.1 GI:1145317
KEYWORDS

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
Marks,J.D.

TITLE Identification of functional and structural amino-acid residues by
paralel mutagenesis
JOURNAL Gene 169 (2), 147-155 (1996)
PUBMED 8647439

REFERENCE 2 (bases 1 to 387)
AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
Marks,J.D.

TITLE Direct Submision
JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA

FEATURES
source location/Qualifiers
1..387

CDS

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ORIGIN

Alignment Scores:

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Pred. No.: 4,77e-76 Length: 387
Score: 700.00 Matches: 129
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0
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US-10-092-640-32 (1-129) x HSU38328 (1-387)

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QY 1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuLysLysProGlyGlnSerLeuLysIle 20
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DB 1 CAGGTGCACACTGTGTGACGTCTGGGGCAGAGTGAACCCGGGAGTCTCTGAAGATC 60
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DB 61 TCTCTGAAGGGTTCTGGATACAGCTTACCAAGTACCTGATCCCTGGGTGGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnLysMetGlyLeuLysTyrProGlyLysSerAspThrLysTyr 60
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DB 121 CCCGGGAAAGCCTGGAGTACATGAGGGCTCATCTATCTGATGACTGACACCAATAT 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
    |||||
DB 181 AGCCCGTCTCTCCAAAGCCAGGTCACCACTCAGTGCACAGTCCGTCAGCACTGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
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DB 241 TTGCATATGAGCAGTGTGAAGCCCTCGGACAGGCCCTGTATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerAsnCysAlaLysTrpProGlyLysPheGlnHisTrpGly 120
    |||||
DB 301 GTGGGATATTGACAGTATGTTCCAACTGCGCAAGTGGCTGAAATACCTTCAGCATTTGGGCG 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
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DB 361 CAGGGTACCCCTGTGACCGTCTCTCA 387
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RESULT 3
LOCUS HSU38331 387 bp mRNA linear PRI 02-OCT-1996
DEFINITION Human anti-c-erbB-2 immunoglobulin heavy chain V-gene, clone
C6PM10.

ACCESSION U38331
VERSION U38331.1 GI:1145323
KEYWORDS

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
Marks,J.D.

TITLE Identification of functional and structural amino-acid residues by
paralel mutagenesis
JOURNAL Gene 169 (2), 147-155 (1996)
PUBMED 8647439

REFERENCE 1 (bases 1 to 387)
 AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
 TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis
 JOURNAL Gene 169 (2), 147-155 (1996)
 PUBMED 8647439
 REFERENCE 2 (bases 1 to 387)
 AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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 /codon_start=1
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 /db_xref="GI:1145324"
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 Pred. No.: 4,77e-76 Length: 387
 Score: 700.00 Matches: 129
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0
 US-10-092-640-32 (1-129) x HSU38331 (1-387)

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 DB 61 TCTGTGAAGGTTCTGATACAGCTTACACAGTACTGATGCTGGGTGGGCGCCAGATG 120
 QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyLysPseSerAspThrLysTyr 60
 DB 121 CCCGGGAAAGCCCTGGAGTACATGGGGCTCATCTTACCTGGTACCTTACACCAATAC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 DB 181 AGCCGCTCTTCCAGAGCCAGGTACCACTTCACTGACAGATGCCCTCCAGACAGCTTAC 240
 QY 81 LeuGlnTrrPseSerLeuLysPseSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 DB 241 TTGCATGAGACAGTCTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
 QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
 DB 301 GTGGGATATTCGACAGTTCCTCAAGTGGCGAAAGTGGCTGAATATTCCTCAGCATTTGGGGC 360
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 DB 361 CAGGATACCTGTCTCCTCTCTCA 387

RESULT 4
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 LOCUS
 DEFINITION Human anti-c-erbB-2 immunoglobulin heavy chain V-gene; clone

CGPM11.
 ACCESSION U38332
 VERSION U38332.1 GI:1145325
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 387)
 AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
 TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis
 JOURNAL Gene 169 (2), 147-155 (1996)
 PUBMED 8647439
 REFERENCE 2 (bases 1 to 387)
 AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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 Pred. No.: 4,77e-76 Length: 387
 Score: 700.00 Matches: 129
 Percent Similarity: 100.0% Conservative: 0
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 US-10-092-640-32 (1-129) x HSU38332 (1-387)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
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 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrrIleAlaTrrValArgIleMet 40
 DB 61 TCTGTGAAGGTTCTGATACAGCTTACACAGTACTGATGCTGGGTGGGCGCCAGATG 120
 QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyLysPseSerAspThrLysTyr 60
 DB 121 CCCGGGAAAGCCCTGGAGTACATGGGGCTCATCTTACCTGGTACCTTACACCAATAC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 DB 181 AGCCGCTCTTCCAGAGCCAGGTACCACTTCACTGACAGATGCCCTCCAGACAGCTTAC 240
 QY 81 LeuGlnTrrPseSerLeuLysPseSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 DB 241 TTGCATGAGACAGTCTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
 QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
 DB 301 GTGGGATATTCGACAGTTCCTCAAGTGGCGAAAGTGGCTGAATATTCCTCAGCATTTGGGGC 360

QY 121 GINGLYTHRLEUVALTHRVALSER 129
 DB 361 CAGGGTACCGTGTGTCACCGTCTCTCA 387

RESULT 5
 LOCUS AR083879 774 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 4 from patent US 5977322.
 ACCESSION AR083879
 VERSION AR083879.1 GI:10010650
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS Marks, J.D. and Schier, R.
 TITLE High affinity human antibodies to tumor antigens
 JOURNAL Patent: US 5977322-A 4 02-NOV-1999;
 FEATURES Location/Qualifiers
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 DB: 2 Gaps: 0

US-10-092-640-32 (1-129) x AR083879 (1-774)

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 DB 121 CCCGGGAAGGCGCTGAGATACATGGGCTCATCTATCTCGTGACTCTGACACCAATATC 180
 QY 61 SERPROSERPHEGLINGLYGINVALTHRILESERVALASPLYSERVALSERTHRALATYR 80
 DB 181 AGCCCGTCTCTTCCAAAGGCAGGTCAACATCTCAGTCGACAAAGTCCGTGACACTGCTTAC 240
 QY 81 LEUGINTPSESRSELEULYSPROSERASPSERALAVALTYRPHCYALAAARGHISASP 100
 DB 241 TTGCATATGAGACAGTCTGAAGCCCTCGACAGCGCGTATATTTTGTCCGAGACATGAC 300
 QY 101 VALGLYTYRCYSESRSESRASNCYSALALYSTTPROGLUTYRPHEGINHISTRPGLY 120
 DB 301 GTGGATATTGCGAGTAGTTCCTCAATCCGCAAGTGGCTGAATACTTCCAGCATTTGGGCG 360
 QY 121 GINGLYTHRLEUVALTHRVALSER 129
 DB 361 CAGGGCACCGTGTGTCACCGTCTCTCA 387

RESULT 6
 AR278815 774 bp DNA linear PAT 10-APR-2003
 LOCUS AR278815
 DEFINITION Sequence 4 from patent US 6512097.
 ACCESSION AR278815
 VERSION AR278815.1 GI:29713203
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 REFERENCE 1 (bases 1 to 774)

AUTHORS Marks, J.D. and Schier, R.
 TITLE High affinity human antibodies to tumor antigens
 JOURNAL Patent: US 6512097-A 4 28-JAN-2003;
 The Regents of the University of California, Oakland, CA
 FEATURES Location/Qualifiers
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 /organism="unknown"
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ALIGNMENT SCORES:
 Pred. No.: 1,15e-75 Length: 774
 Score: 700.00 Matches: 129
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-092-640-32 (1-129) x AR278815 (1-774)

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 QY 21 SERCYSLYSGLYSERGLYTYRSERPHERSERTYRTPILAEATRPVALARGINMET 40
 DB 61 TCCTGTAAAGGGTTCTGGATACAGCTTTACCACTACTGATCGCTGGGTGGCCAGATG 120
 QY 41 PROGLYLSGLYLEUGLUTYRMETGLYLEULIETLYRPROGLYASPSERASPHRYLSITYR 60
 DB 121 CCCGGGAAGGCGCTGAGATACATGGGCTCATCTATCTCGTGACTCTGACACCAATATC 180
 QY 61 SERPROSERPHEGLINGLYGINVALTHRILESERVALASPLYSERVALSERTHRALATYR 80
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 DB 301 GTGGATATTGCGAGTAGTTCCTCAATCCGCAAGTGGCTGAATACTTCCAGCATTTGGGCG 360
 QY 121 GINGLYTHRLEUVALTHRVALSER 129
 DB 361 CAGGGCACCGTGTGTCACCGTCTCTCA 387

RESULT 7
 AF516873 1509 bp mRNA linear SYN 01-MAR-2004
 LOCUS AF516873
 DEFINITION Synthetic construct membrane-acting immunotoxin fusion protein
 mRNA, complete cds.
 ACCESSION AF516873
 VERSION AF516873.1 GI:31324248
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 1509)
 Gurtan, C. and Ellar, D.J.
 TITLE Design and construction of membrane-acting immunotoxins based on the Bacillus thuringiensis delta-endotoxin Cyt2AaI for expression in Pichia pastoris
 Med. Microbiol. Immunol. (Berl.) 189, 37-37 (2000)
 JOURNAL Expression in Pichia pastoris and purification of a membrane-acting immunotoxin based on a synthetic gene coding for the Bacillus thuringiensis Cyt2AaI toxin
 REFERENCE Protein Expr. Purif. 29 (1), 103-116 (2003)
 JOURNAL 12729731
 PUBMED 12729731
 REFERENCE 3 (bases 1 to 1509)

AUTHORS Gurkan, C. and Ellar, D.J.
 TITLE Expression of the Bacillus thuringiensis Cyt2Aa1 toxin in Pichia
 JOURNAL pastoris using a synthetic gene construct
 PUBLISHED Biotechnol. Appl. Biochem. 38 (Pt 1), 25-33 (2003)
 REFERENCE 12628007
 4 (bases 1 to 1509)
 AUTHORS Gurkan, C., Ellar, D.J. and Marks, J.
 TITLE Direct Submision
 JOURNAL Submitted (30-MAY-2002) Department of Biochemistry, University of
 Cambridge, 80 Tennis Court Road, Old Addenbrooke's Site, Cambridge
 CB2 1GA, England

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 Query Match: 99.6% Indels: 0
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QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaAaGHisAsp 100
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 QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
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RESULT 8
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 C6PM12.
 C6PM12.
 U38333
 U38333.1 GI:1145327
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 387)
 Schier, R., Ballint, R.F., McCall, A., Apell, G., Larrick, J.W. and
 Marks, J.D.
 Identification of functional and structural amino-acid residues by
 parsimonious mutagenesis
 Gene 169 (2), 147-155 (1996)
 8647439
 2 (bases 1 to 387)
 Schier, R., Ballint, R.F., McCall, A., Apell, G., Larrick, J.W. and
 Marks, J.D.
 Direct Submision
 Submitted (11-Oct-1995) Robert Schier, Anesthesia, UC San
 Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
 Location/Qualifiers
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 Query Match: 99.1% Indels: 0
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US-10-092-640-32 (1-129) x HSU38333 (1-387)

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 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
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QY      61  SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrIleTyr 80
Db      181  AGCCGCTCTTCCAGAGCCAGGTGACCATCAGTGCAGAGTCCGTCCAGCATGCTTAC 240
QY      81  LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db      241  TTGCATGGAGAGCTGTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
QY      101  ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
Db      301  GTGGGATATTGGAGATGATTCACCACTGGCGCAAGTGGCTGAAATATCTTCAGCATTTGGGGC 360
QY      121  GlnGlyThrLeuValThrValSerSer 129
Db      361  CAGGGCACCCCTGGTCAACGCTCTCTCA 387

RESULT 9
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LOCUS      Human anti-c-erbB-2 immunoglobulin heavy chain V mRNA, partial cds,
DEFINITION  U38330
VERSION      U38330.1 GI:1145321
KEYWORDS
SOURCE
ORGANISM    Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 387)
REFERENCE   Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
AUTHORS    Marks, J.D.
TITLE      Identification of functional and structural amino-acid residues by
JOURNAL     parsimonious mutagenesis
PUBMED      Gene 169 (2), 147-155 (1996)
8647439
2 (bases 1 to 387)
REFERENCE   Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
AUTHORS    Marks, J.D.
TITLE      Direct Submision
JOURNAL     Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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ORIGIN
Alignment Scores:
Pred. No.:      4,56e-75      Length:      387
Score:          692.00      Matches:      127
Percent Similarity: 99.2%      Conservative: 1
Best Local Similarity: 98.4%      Mismatches: 1
Query Match:    98.9%      Indels:      0
DB:             5      Gaps:      0
US-10-092-640-32 (1-129) x HSU38330 (1-387)

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QY      21  SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTyrValArgIleMet 40
Db      61  TCCTGTAAAGGTTCTGGATACAGCTTTACAGACTTCTGGATGCTGGGTGGCCAGATG 120
QY      41  ProGlyLysGlyLeuGluTyrMetGlyLeuLeuTyrProGlyAspSerAspThrLysTyr 60
Db      121  CCGGGGAAAGGCGCTGGAGTACATGGGGCTCATCTATCCGTGGATTCGATACCAATAC 180
QY      61  SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrIleTyr 80
Db      181  AGCCGCTCTTCCAGAGCCAGGTGACCATCAGTGCAGAGTCCGTCCAGCATGCTGCTAC 240
QY      81  LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db      241  TTGCATGGAGAGCTGTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
QY      101  ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
Db      301  GTGGGATATTGGAGATGATTCACCACTGGCGCAAGTGGCTGAAATATCTTCAGCATTTGGGGC 360
QY      121  GlnGlyThrLeuValThrValSerSer 129
Db      361  CAGGGTACCCCTGGTCAACGCTCTCTCA 387

RESULT 10
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LOCUS      Human anti-c-erbB-2 immunoglobulin heavy chain V mRNA, partial cds.
DEFINITION  U38224
VERSION      U38224.1 GI:1145299
KEYWORDS
SOURCE
ORGANISM    Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 387)
REFERENCE   Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
AUTHORS    Marks, J.D.
TITLE      Identification of functional and structural amino-acid residues by
JOURNAL     parsimonious mutagenesis
PUBMED      Gene 169 (2), 147-155 (1996)
8647439
2 (bases 1 to 387)
REFERENCE   Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
AUTHORS    Marks, J.D.
TITLE      Direct Submision
JOURNAL     Submitted (07-OCT-1995) Ronert Schier, Anesthesia, UC San
Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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Pred. No.:      1,06e-74      Length:      387
Score:          689.00      Matches:      127

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Percent Similarity: 99.2% Conservative: 1
 Best Local Similarity: 98.4% Mismatches: 1
 Query Match: 98.4% Indels: 0
 DB: 5 Gaps: 0

US-10-092-640-32 (1-129) x HSU38224 (1-387)

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QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTripleAlaTrpValArgGlnMet 40
DB      61 TCCTGTAAAGGTTCCGGATACAGCTTACAGCTACGATCCCTGGGCGCCAGATG 120
QY      41 ProGlyLysGlyLeuGlnLysTyrMetGlyLeuLysIleTyrProGlyAspSerAspThrLysTyr 60
DB      121 CCGGGAAAGGCTGGAGTACATGGGGCTCATCTATCTGTGATTCTGATACCAATAC 180
QY      61 SerProSerPheGlnGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB      181 AGCCCTCTCTCCCAAGGCCAGGTCACCATCTCAGTGCACAAGCCGTCAGCAGCTGCCTAC 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB      241 TTGCATGAGACAGCATGTCGAGCCCTCGACAGCCCGCTGATTTTGTGCGAAGATGAC 300
QY      101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTrpProGlyLysPheGlnHisTrpGly 120
DB      301 GTGGGATATTGTCAGTATTCACACTGCGCAAGTGGCCTGAATACCTTCGACATGGGGC 360
QY      121 GlnGlyThrLeuValThrValSerSer 129
DB      361 CAGGGCACCTGTGTCACCGTCTCTCA 387

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RESULT 11
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 LOCUS Human anti-c-erbB-2 immunoglobulin heavy chain V mRNA, partial cds,
 DEFINITION clone C6PM2.
 ACCESSION U38323
 VERSION U38323.1 GI:1145307
 KEYWORDS

SOURCE
 ORGANISM Homo sapiens (human)

Homosapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 387)

REFERENCE
 AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and

TITLE Identification of functional and structural amino-acid residues by

JOURNAL parisonious mutagenesis
 PUBMED Gene 169 (2), 147-155 (1996)
 REFERENCE 8647439

AUTHORS 2 (bases 1 to 387)
 Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
 Marks,J.D.
 DIRECT SUBMISSION

TITLE Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
 JOURNAL Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
 FEATURES Location/Qualifiers

source

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ORIGIN

Alignment Scores:

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Query Match: 98.3% Indels: 0
DB: 5 Gaps: 0

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US-10-092-640-32 (1-129) x HSU38323 (1-387)

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QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTripleAlaTrpValArgGlnMet 40
DB      61 TCCTGTAAAGGTTCCGGATACAGCTTACAGCTACGATCCCTGGGCGCCAGATG 120
QY      41 ProGlyLysGlyLeuGlnLysTyrMetGlyLeuLysIleTyrProGlyAspSerAspThrLysTyr 60
DB      121 CCGGGAAAGGCTGGAGTACATGGGGCTCATCTATCTGTGATTCTGATACCAATAC 180
QY      61 SerProSerPheGlnGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB      181 AGCCCTCTCTCCCAAGGCCAGGTCACCATCTCAGTGCACAAGCCGTCAGCAGCTGCCTAC 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB      241 TTGCATGAGACAGCATGTCGAGCCCTCGACAGCCCGCTGATTTTGTGCGAAGATGAC 300
QY      101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTrpProGlyLysPheGlnHisTrpGly 120
DB      301 GTGGGATATTGTCAGTATTCACACTGCGCAAGTGGCCTGAATACCTTCGACATGGGGC 360
QY      121 GlnGlyThrLeuValThrValSerSer 129
DB      361 CAGGGCACCTGTGTCACCGTCTCTCA 387

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RESULT 12
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 LOCUS Human anti-c-erbB-2 immunoglobulin heavy chain V mRNA, partial cds,
 DEFINITION clone C6PM8.
 ACCESSION U38329
 VERSION U38329.1 GI:1145319
 KEYWORDS

SOURCE
 ORGANISM Homo sapiens (human)

Homosapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 387)

REFERENCE
 AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and

TITLE Identification of functional and structural amino-acid residues by

JOURNAL parisonious mutagenesis
 PUBMED Gene 169 (2), 147-155 (1996)
 REFERENCE 8647439

AUTHORS 2 (bases 1 to 387)
 Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
 Marks,J.D.
 DIRECT SUBMISSION

TITLE Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
 JOURNAL Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
 FEATURES Location/Qualifiers

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CDS

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ORIGIN

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Best Local Similarity:	98.4%	Mismatches:	2
Query Match:	97.7%	Indels:	0
DB:	5	Gaps:	0

US-10-092-640-32 (1-129) x HSU38329 (1-387)

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QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
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QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTyrIleAlaTyrValArgGlnMet 40
    |||||
DB 61 TCCTGTAAGGGTTCTGGATACAGCTTTACAGCTACTGATGCGCTGGGTGGCCAGAG 120
QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
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DB 121 CCCGGGAAAGGCTGGAGTACATGGGGCTCATCTATGCTGGGAGATCTCTCAACCAATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
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DB 301 GTGGATATTTGCAGTATGTTCCAACTGCGGAAAGTGGCTGTAATCTTCCAGCATTTGGGCG 360
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DB 361 CAGGGTACCTGTGTACCGTCTCTCTCA 387

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RESULT 13

HSU38327 387 bp mRNA linear PRI 02-OCT-1996
 LOCUS Human anti-c-erbB-2 immunoglobulin heavy chain V mRNA, partial cds,
 clone C6PM6.
 DEFINITION U38327
 ACCESSION U38327.1 GI:1145315
 VERSION
 KEYWORDS
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 387)
 Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
 Marks, J.D.
 Identification of functional and structural amino-acid residues by
 parthenogenesis mutagenesis
 Gene 169 (2), 147-155 (1996)
 JOURNAL PUBLISHED 8647439
 2 (bases 1 to 387)
 Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
 Marks, J.D.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBLISHED
 2 (bases 1 to 387)
 Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
 Marks, J.D.

Mark, J.D.
 Direct Submission
 Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
 Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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 location/Qualifiers
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CDS

Alignment Scores:

Pred. No.:	5,776-74	Length:	387
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Percent Similarity:	97.7%	Conservative:	0
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ORIGIN

US-10-092-640-32 (1-129) x HSU38327 (1-387)

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DB 361 CAGGGTACCTGTGTACCGTCTCTCTCA 387

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 ACCESSION U38334.1 GI:1145329
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 387)
 Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
 Marks, J.D.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBLISHED
 2 (bases 1 to 387)
 Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
 Marks, J.D.

AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis
JOURNAL Gene 169 (2), 147-155 (1996)
PUBMED 8647439
REFERENCE 2 (bases 1 to 387)
AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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ORIGIN
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US-10-092-640-32 (1-129) x HSU8334 (1-387)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
DB 1 CAGGTCAAGCTGTTGACGCTGGGGCAGAGTTGAAGAAGCCGGGAGATCTCGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
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QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
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QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGTACCTGTGTCAACCGTCTCTCA 387
RESULT 15
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DEFINITION Human anti-c-erbB-2 immunoglobulin heavy chain v region mRNA,
partial cds.
ACCESSION U36543

VERSION U36543.1 GI:1145225
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 387)
AUTHORS Schier, R., Bye, J., Apell, G., McCall, A., Adams, G.P., Weiner, L.W. and Marks, J.D.
TITLE Isolation of high affinity monomeric Human anti-c-erbB-2 single chain Fv using affinity driven selection
JOURNAL J. Mol. Biol. (1995) In press
REFERENCE 2 (bases 1 to 387)
AUTHORS Schier, R.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1995) Robert Schier, Anesthesia, University of California at San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
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ORIGIN
Alignment Scores:
Pred. No.: 7.66e-74 Length: 387
Score: 682.00 Matches: 123
Percent Similarity: 100.0% Conservative: 6
Best Local Similarity: 95.3% Mismatches: 0
Query Match: 97.4% Indels: 0
Gaps: 0
DB: 5
US-10-092-640-32 (1-129) x HSU8334 (1-387)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
DB 1 CAGGTCAAGCTGTTGACGCTGGGGCAGAGTTGAAGAAGCCGGGAGATCTCGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
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QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
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QY 81 LeuGlnTyrSerSerLeuLysPheSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 TTGCAATGAGCAGCTGTGAAGCCCTCGACAGCGCGGTGATTTTGTGGGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB 301 GTGGGATATTGACAGTATGTTCCAACTGCGCAAGTGGCTGAATATCTTCCAGCATTTGGGCG 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
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